

; TITLE: 008)									
; JOURNAL: Plant Physiol.									
; VOLUME: 113									
; ISSUE: 1									
; PAGES: 306-306									
; DATE: 1997-01-01									
; DATABASE ACCESSION NUMBER: genbank/X94938									
; DATABASE ENTRY DATE: 1998-02-13									
; RELEVANT RESIDUES: (1)..(1636)									
US-10-764-138-6									
Query Match 100.0%; Score 1636; DB 21; Length 1636;									
Best Local Similarity 100.0%; Pred. No. 7, 4e-311;									
Matches 1636; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	TTTACTCTTT	CAGTGAGAGAGAGAGT	TAGAGCTGT	AAAAAGCACATG	ACTTCGATACCAT	60		
DB	1	TTTACTCTTT	CAGTGAGAGAGAGT	TAGAGCTGT	AAAAAGCACATG	ACTTCGATACCAT	60		
QY	61	TGGGGCTCT	CAGCCTCCGTC	TTTGTAGCTCCT	CAGCGCGGCATCTT	CACGGCGGAGATT	120		
DB	61	TGGGGCTCT	CAGCCTCCGTC	TTTGTAGCTCCT	CAGCGCGGCATCTT	CACGGCGGAGATT	120		
QY	121	CTTTGAAACG	TGTCCTCCGATATAGAC	CAACGCAAGGAAATGT	CTGCTGCTGTTATAGAA	180			
DB	121	CTTTGAAACG	TGTCCTCCGATATAGAC	CAACGCAAGGAAATGT	CTGCTGCTGTTATAGAA	180			
QY	181	GAATGATGCT	GTACCGGTACATTAAT	TTTACTACAAATG	GAGCAAAAATGGTGAAC	240			
DB	181	GAATGATGCT	GTACCGGTACATTAAT	TTTACTACAAATG	GAGCAAAAATGGTGAAC	240			
QY	241	CTAAACAGAC	CATTAGTGTACATGCGCGG	CAAGCTGTGTCGAA	CAGGATCATTCGGAATTG	300			
DB	241	CTAAACAGAC	CATTAGTGTACATGCGCGG	CAAGCTGTGTCGAA	CAGGATCATTCGGAATTG	300			
QY	301	TATTCAGGCA	AAATGCTTTGGAAC	TGGAGAATCAGT	TAGCCATTAAGAAGGTTT	TGCAAG	360		
DB	301	TATTCAGGCA	AAATGCTTTGGAAC	TGGAGAATCAGT	TAGCCATTAAGAAGGTTT	TGCAAG	360		
QY	361	ATCGCGGTTA	TAAAAACCGAGAGT	TGCAATTAATGCGAC	TAAATGGACCATCAAAATGTGG	420			
DB	361	ATCGCGGTTA	TAAAAACCGAGAGT	TGCAATTAATGCGAC	TAAATGGACCATCAAAATGTGG	420			
QY	421	TTTCTCTTGA	GCATCTGTTCTCTAC	CAACGACTAGAGAT	GAGCTCTTCTCAATCTCG	480			
DB	421	TTTCTCTTGA	GCATCTGTTCTCTAC	CAACGACTAGAGAT	GAGCTCTTCTCAATCTCG	480			
QY	481	TTATGGAGTA	TGTACAGAGACAT	TGTACCGGGTTT	TGAAGCACTATAGTTCAAACC	540			
DB	481	TTATGGAGTA	TGTACAGAGACAT	TGTACCGGGTTT	TGAAGCACTATAGTTCAAACC	540			
QY	541	AGCGGATGCT	TATCTTCTATGTCA	AACTTTACACATAC	CAAAATCTTTCAGAGGCTTGGCTT	600			
DB	541	AGCGGATGCT	TATCTTCTATGTCA	AACTTTACACATAC	CAAAATCTTTCAGAGGCTTGGCTT	600			
QY	601	ATATCCATA	CTGCTCTGTTGTCG	CCACAGATATAAA	CCACAAAATCTTTTGGTTG	660			
DB	601	ATATCCATA	CTGCTCTGTTGTCG	CCACAGATATAAA	CCACAAAATCTTTTGGTTG	660			
QY	661	ATCCCCACAC	CCCATCAGTGTAA	AGCTCTGTGATTT	TGGAAGTGCAAAAGTACTGGTGAAG	720			
DB	661	ATCCCCACAC	CCCATCAGTGTAA	AGCTCTGTGATTT	TGGAAGTGCAAAAGTACTGGTGAAG	720			
QY	721	GTGAACCAAC	ACATATATATCT	CTCGGTATTA	CCGAGCTCAGAACTCATCTTTG	780			
DB	721	GTGAACCAAC	ACATATATATCT	CTCGGTATTA	CCGAGCTCAGAACTCATCTTTG	780			
QY	781	GTCCCAAGAG	TATACATCATCA	TTCATTTGATAT	TGTTCTGCGCAGAGC	840			
DB	781	GTCCCAAGAG	TATACATCATCA	TTCATTTGATAT	TGTTCTGCGCAGAGC	840			
QY	841	TACTTCTGG	CGACCGCTTAT	TCCCGGAGAAA	ATTCTGTGGACCA	GCTAGTGGAGATCA	900		

RESULT 2
US-10-292-408-25
; Sequence 25, Application US/10292408
; Publication No. US20030182692A1
; GENERAL INFORMATION:
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: DA COSTA E SILVA, OSWALDO
; APPLICANT: CHEN, RUOYING
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METHODS
; TITLE OF INVENTION: OF USE IN PLANTS
; FILE REFERENCE: 16313-0178
; CURRENT FILING DATE: 2002-11-12
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25

Db 556 TGAGAGCTGTATCGAGTTCTGAAACATATATAGTAGTGCAAAACCAAGAAATGCCTCTGT 615
Qy 557 CTATGTCRAACTTACACATACCAATCTTCAGAGCTTGGCTTATATCCATCTGCTCC 616
Db 616 CTATGTTAACTTTACATGATCAGATCTTCGGGGACTTGTCTTCAATTCACAAATGTTGC 675
Qy 617 TGGTGTCTGCCACAGAGATATAAAACCAACAAATCTTTTGGTTGATCCCCACACCCATCA 676
Db 676 TGGAGTTTGTACAGAGATCTAAGGCTCBAATCTTCTGTTGATCCCTTACTCATCA 735
Qy 677 GTGTAAGCTCTGTGATTTTGGAGTGCAGAAAGTACTGTTGTAAGGTGAACCAAAATATC 736
Db 736 AGTCMAAATCTGTACTTTGGCAGTTCGAAACAGCTCGTTAAAGGTGAAGCCAAATTTTC 795
Qy 737 ATATATCTGCTCTCGGTATACCGAGCTCCAGAACATCTCTTGGTGCCACAGAGATATAC 796
Db 796 TTACATCTGCTCACGATTTACCGTGCAACCCGAGCTCATATTTGGTGCCACAGTATAC 855
Qy 797 ATCATCCATTTGATATGCTGCTGTTGTGTTCTGGCAGAGCTACTTCTTGGGCAGCC 856
Db 856 AACTTCTATGATATCTGCTGCTGTTGTGTTCTTGTGAGCTTCTTCTTGGTCAAGCC 915
Qy 857 GTTATTCGGGAGAAATCTGTGCAACAGCTAGTGGAGATCATAAAGTTCTTGGTAC 916
Db 916 ATTATTTCCGGGAGAAATGCTGTGATCAGCTCGTTGAAATTTATAAAGTTCTTGGTAC 975
Qy 917 TCCAACTCCGGAAGAAATCCGGTGATGCAACCCAACTACACAGACTTCAGATTTCCACA 976
Db 976 ACCAACTCCGGAAGAAATCCGGTTGATGAATCCACATTTACACAGATTTTCAGGTTTCCACA 1035
Qy 977 AATCAAGGCCACCTTGGCATAAAGTTTTCACAGCGGATGCCCTCCGGAAGCCATTTGA 1036
Db 1036 GATTAAGGCACATCCCTGGCACAAGATCTTCACAAAGAGTGCCCCACAGAGCGATTGA 1095
Qy 1037 CTTGCACTCTCGCTTCTTCAATACTCACCAAGTCTACGTGCACTGCGCTCGAGGCATG 1096
Db 1096 TTTTGCACTCAAGGCTGCTTCAATCTCTCAAGTCTAAGATGACACAGCGCTCGAAGCTTG 1155
Qy 1097 TGGGATCCGTTTTCATGAACTCCGTGAGCCAAATGCTCGTCTTCCAAATGGCCGACC 1156
Db 1156 TGCAATCCGTTCTTCAATGAACTCAGAGAACCAACCGCTCGTTTACCAAAATGGACGGCC 1215
Qy 1157 TCTACCAACCGTTTCAACTTCAACAAAGATGTTCTGGGGCTTACCGGAGCTTATCAA 1216
Db 1216 TTTCCGCTCTCTTCAATCTTCAACAAAGATGTTCTGGATCATCACTGAATGTTGCTAA 1275
Qy 1217 CAGGCTAATACAGAGATGTGAGGCGACAGATGAATGGTGGCTTTCATTTCAAGCTGG 1276
Db 1276 CAAGTTGATTCAGAGACCATATCAAGAGACAAATGGGCTTAAGCTTCTTGAATCAATCTGG 1335
Qy 1277 ACCCTAGAA 1285
Db 1336 AACTTAAAA 1344

RESULT 4
US-09-938-842A-875
; Sequence 875, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 875
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-875

Query Match 44.7%; Score 730.8; DB 9; Length 1143;
Best Local Similarity 77.5%; Pred. No. 2.1e-133;
Matches 885; Conservative 0; Mismatches 257; Indels 0; Gaps 0;

Qy 141 ATAGCAACGACGACGAAATGTCTGCTGTATATAGAGGAAATGATGCTGTACCCTG 200
Db 1 ATGGCTGATGATAGAGATGCTGCTGCTGTAGTTGATGGACATGATCAAGTCACTGT 60
Qy 201 CACATAATTTCTACTACAAATGGAGGCAAAATGTTGAACCTTAAACAGACCAATTAATTAC 260
Db 61 CATATTATTTCCACCACAAATCGTGGCAAAATGTTGAACCAAAACAGACAAATTAATTAC 120
Qy 261 ATGGCGGAACGTTGTTGGAAACAGATCAATTCGGAATTTGTAATCCAGGCAAAATCTGTG 320
Db 121 ATGGCGGAGCGAGTTGTTGGTACAGGCTGTTCCGGATCGTTTCCAGCAAAATGTTTG 180
Qy 321 GAACTTGGAGAAATCAGTAGCCATTAAGAAGGTTTTCAGAGATCGCCGTTTATAAAAAACCGA 380
Db 181 GAGACTGGAGAAACCGTGGCGATTAAGAAGGTTTTCAGAGATAGAAGATACAGAACCGA 240
Qy 381 GAGTTGCAATTAATGCGACTAAATGGACCAATCAAAATGTTGGTTTCTTGAAGCAATTTGTC 440
Db 241 GAACTTCACTGATGCTGATGATGATCATCCGAATGTTGTTGTTGAAGCAATTTGCTTC 300
Qy 441 TTCTCTACAACTAGAGATGAGCTCTTCTCAATCTGTTATGAGATGTTACACAGAG 500
Db 301 TTTTGCAGCTACAAGTAAGAAGCGAGCTTTCTTGAACCTTGGTTATGAGATGTTCCCTGAG 360
Qy 501 ACATTTGATCCGGTTTGAAGCACTATACCTAGTTTCAAAACAGCGGATGCTATCTTCTAT 560
Db 361 AGCTTGTATCGAGTTCTGAAACATATATAGTAGTGCAAAACCAAGATGCTCTTGTCTAT 420
Qy 561 GTCAAACTTTACACATACCAAAATCTTTCAGAGGTTGGCTTTATCATCTGCTCTCTGT 620
Db 421 GTTAAACTTTACATGATCAGATCTTCCGGGACTTGTCTTCAATTCACAAATGTTGCTGGA 480
Qy 621 GTCTGCCACAGAGATATAAAACCAAAATCTTTGGTTGATCCCCACACCCATCAAGTGT 680
Db 481 GTTTGTGCACAGAGATCTAAAGCCTCAAAATCTTCTGGTTGATCCTCTTACTCATCAATC 540
Qy 681 AAGCTCTGTGATTTTGGAAAGTACAAAGTACTGGTGAAAGGTGAACCAACATATCATAT 740
Db 541 AAAATCTGTGACTTTGGCAGTGGAAACAGCTCGTTAAAGGTGAAGCAACATTTCTTAC 600
Qy 741 ATCTGCTCTCGGTAATACCGAGCTCAGAACTCATCTTTGGTGCCACAGAGTATATCA 800
Db 601 ATCTGCTCAGATTTCTACCGTGACCCGAGCTCATATTTGGTGCCACTGAGTACACAACT 660
Qy 801 TCCATTTGATATGCTGCTGCTGTTGTTCTGGCAGAGCTACTTCTTGGGAGCGGTTA 860
Db 661 TCTATTGATATCTGGTCTGCTGTTGTTCTTGGTGAGGCTTCTTCTTGGTGAGCCATTA 720
Qy 861 TTCCCGGAGAGAAATCTCTGTGGACAGCTAGTGGAGATCATAAAGGTTCTTGTGATCTCCA 920
Db 721 TTTCCCGGAGAGAAATGCTGTGGATCAGCTCGTTGAAATTTATAAAGTCTTGTGTACACCA 780
Qy 921 ACTTCGGAAGAAATCCGGTGCATGAACCAAACTACACAGACTTCAGATTTCCCAAAATC 980
Db 781 ACTTCGGAAGAAATCCGGTGTATGAATCCACATTCACAGATTTCCAGGTTTCCACAGATA 840
Qy 981 AAAGCCCAACCTTGGCATAGGTTTTCACAGCGGATGCTCTCCGGAAGCAATTTGACCTT 1040
Db 841 AAGGCACATCCCTGGGCACAGAGATCTTCCCAAAAGGATGCCCCCAAGGATTTGATTTT 900

QY 1041 GCATCTCGGCTTCTTCAATACCTACCAAGTCTACGTTGACGCTGCGCTCGAGGCATGTGGC 1100
DB 901 GCATCAAGGCTGCTTCAATACCTACCTCAAGTCTAAGATGACAGCGCTCGAAGCTTGTGCA 960
QY 1101 CATCGGTTTTCAATGAACCTCGGTGAGCAAAATGCTCGTCTTCCAAATGGCCGCACTCTA 1160
DB 961 CATCGGTTTTCAATGAACCTCAGAGAACCAACGCTCGTTACCAAAATGGACGGCTTTC 1020
QY 1161 CCACGGTGTTCATCTTCAAAAGAGTGTCTGGGGTTCACCGAGCTTATCAACAGG 1220
DB 1021 CCGGCTCTCTTCAACTTCAAAAGAGTGTCTGGGATCATCACTGAACTGGTCAACAG 1080
QY 1221 CTAATACAGAGCTGTGAGGCGACAGATGAATGGTCTTCCATTTCAAGCTGACCC 1280
DB 1081 TTGATTCAGACCATATCAAGAGACAATTTGGGTCTAAGCTTCTTGAATCAATCTGAACT 1140
QY 1281 TA 1282
DB 1141 TA 1142

RESULT 5
US-09-938-842A-875
; Sequence 875, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; FILE REFERENCE: SAME, AND METHODS OF USE
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 875
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-875

Query Match 44.7%; Score 730.8; DB 11; Length 1143;
Best Local Similarity 77.5%; Pred. No. 2.1e-133;
Matches 885; Conservative 0; Mismatches 257; Indels 0; Gaps 0;

QY 141 ATAGACAACGACAGCAAGAAATGCTGCTGCTGTATAGAGGAAATGATGCTGTACCGGT 200
DB 1 ATGGCTGATGATAGAGAGATGCTGCTGCTGTAGTTGATGGACATGATCAAGTCACTGT 60
QY 201 CACATAATTTCTACTACAAATTTGAGGCAAAAATGGTGAACCTTAAACAGACCACTTAGTTAC 260
DB 61 CATATTAATTTCCACCACAATCGTGGCAAAAATGGTGAACCAACACAGCAATTAGTTAC 120
QY 261 ATGGCGGAACGTTGTTGGAAACAGATCATTCGGAATTTGATTCAGGCAAAATGCTTG 320
DB 121 ATGGCGGAGCGAGTTGTTGGTACAGGCTGTTTCGGGATCGTTTCCAAAGCAAAATGTTG 180
QY 321 GAACTGGAGATCAGTACCAATTAAGAGGTTTTCAGATCGCGGTTTATAAACAACGA 380
DB 181 GAGACTGGAGAACCGTGGCGATAAAGAGGTTTTCAGATGAGAATGATCAAGAACCGA 240
QY 381 GAGTTGCAATTAATGCAATTAATGAGCAATTCGAAATGTTTCCCTTGAAGCAATTTGTTTC 440
DB 241 GAACTCAGTTGATGCTGTGATGATCATCCGAATGTTGTTTGAAGCAATTTGTTTC 300
QY 441 TTCTCTACAAACGACTAGAGATGAGCTCTTCTCTCAATCTCGTTATGGAGTATGTACACAG 500

RESULT 6

US-10-424-599-124786
; Sequence 124786, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kowalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599

DB 301 TTTTGCATCAAGTAAAGACGAGCTTTTCTTGAACCTTGGTTATGAGATATGTCCTGAG 360
QY 501 ACATTGTACCGGTTTTGAAGCACTATAGTTTCAAAACCGCGGATCCCTATCTTCTAT 560
DB 361 AGCTTGATCGAGTTCTGAAACATTTATAGTAGTCAAAACCAAGAAATGCTCTTGTCTAT 420
QY 561 GTCAAACTTTACACATCAAAATCTTTCAGAGGCTTGGCTTATATCCATCTGCTCTGTGT 620
DB 421 GTTAAACTTTATCATGTATCAGATCTTTCGGGAGCTTGTCTTACATTCACAAATGTTGTGGA 480
QY 621 GTCTGCCACAGAGATATAAAACCAAAATCTTTTGGTTGATCCCAACACCCATCAGTGT 680
DB 481 GTTGTTCACAGAGATCTAAAGCTCAAAATCTTCTGGTTGATCCTTCTTACTCATCAAGTC 540
QY 681 AAGCTCTGTGTATTTTGGAGTGCMAAAGTACTGTGTGAAGGTGAACCAAAACATATCATAT 740
DB 541 AAAATCTGTGACTTTGGCAGTGGCAAAACAGCTCGTTAAAGGTGAAGCCAAACATTTCTTAC 600
QY 741 ATCTGCTCTCGGTATTTACCGAGCTCCAGAACTCATCTTTTGGTGCCACAGAGTATACATCA 800
DB 601 ATCTGCTCACGATTTCTACCGTGCACCGAGCTCATATTTTGGTGCCACTGAGTACACAACT 660
QY 801 TCCATTGATATATGCTGCTGCTGTTGCTGTTCTGGCAGAGTACTTCTTGGGCGAGCGTTA 860
DB 661 TCTATTGATATCTGCTGCTGCTGTTGTTCTTGTCTGAGCTTCTTCTTGGTCAGGCATTA 720
QY 861 TTCCCGGAGAGAAATTTCTGTGGACCCAGCTAGTGGAGATCATAAAGGTTCTTGGTACTCCA 920
DB 721 TTTCCCGAGAGAAATGCTGTGGATCAGCTCGTTGAAATTAATAAAGTTCTTGGTACACCA 780
QY 921 ACTCGCGAAGAAATTCGGTGATGAAACCCAACTACACAGACTTCAGATTTCCCAAAATC 980
DB 781 ACTCGAGAGAAATCCGTTGTATGAATCCACATTAACAGATTTTCAAGGTTTCCACAGATA 840
QY 981 AAAGCCCACTTGCATAAGSTTTTCCACAGCGGATGCTTCCGAGAGCCATTCACCTT 1040
DB 841 AAGGCACATCTCCCTGGCACAAGATCTTCCAAAAGATGCCCCCAAGAGCGATTTGATTTT 900
QY 1041 GCATCTCGGCTTCTTCAATATCTCACCAAGTCTACGTTTGCACCTCGCGCTCGAGGCATGTGG 1100
DB 901 GCATCAAGGCTGCTTCAATATCTTCCAAGTCTAAGATGACAGCGCTCGAAGCTTGTGCA 960
QY 1101 CATCGTTTTCAATGAACCTCGGTGAGCAAAATGCTGCTTCCAAATGGCGCACTCTA 1160
DB 961 CATCGTTCTTTGATGAATCAGAGAACCAACGCTCGTTTACCAAAATGGACGGCTTTC 1020
QY 1161 CCACGGTGTTCAACTTCAAAACAGAGTGTGCTGGGCTTCCACCGAGCTTATCAACAGG 1220
DB 1021 CCGCTCTCTTCAACTTCAAAACAGAGAGTGTGATCATCACCTGAACTGGTCAACAG 1080
QY 1221 CTAATACAGAGCATGTGAGGCGACAGATGAATGGTGGCTTTCATTTCAAGCTCGACCC 1280
DB 1081 TTGATTCAGACCATATCAAGAGACAATTTGGGTCTAAGCTTCTTGAATCAATCTGGAAT 1140
QY 1281 TA 1282
DB 1141 TA 1142

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; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 124786
; LENGTH: 2519
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_83691C.1
US-10-424-599-124786

Query Match
  44.3%; Score 724.6; DB 18; Length 2519;
Best Local Similarity 78.3%; Pred. No. 4.7e-132;
Matches 907; Conservative 0; Mismatches 249; Indels 3; Gaps 3;

QY 129 CGTCGTCGATATAGACACGACGAGGAATGCTGCTGCTGTTATAGAGGAATGAT 188
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 775 CGGAGTCGATATGAGACCGGATAGGATATGTCAGCTACTGTCAATGAGGGGAATGAT 834
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 189 GCT-GTTACCGGTACATAATTTCTACTACAATTTGGAGGCAAAAATGGTGAACCTTAAACA 247
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 835 GCAGGTACTGGCCACATAATCTCCACCACAAATTTGGAGCNAAAAATGGGNAACCTTAAACA 894
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 248 GACCATATGTTACATGCGCGAAGCTGTTGTTGGAACAGGATCATTCGGAATTTGATTTCA 307
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 895 GACCATCAGTTACATGGCAGAACGCTGTTGTTGGCACTGGATCATTTGGAGTTGTTTCCA 954
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 308 GGCANAATGCTGGAACTG-GAGATCAGTAGCCCAATTAAGAGGTTTTCGAAGATCGC 366
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 955 GGCANAATGCTGGAGACTGCGAGAGCGAGTGCTATTAAGAAAGGTCCTTGCAGACAGCG 1014
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 367 GTTATAAAAACCGAGAGTTGCAATTAATGCGACTAATGGAACCAATCAAAATGTGTTTCT 426
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1015 GATACAAAATCGAGAATTCGAGTTAATGCGCTTAATGATCATCCCAATCAACTTACA 1074
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 427 TGAAGCATTTGTTCTCTACAAAGCTAGAGAT-GAGCTTCTCCTCAATCTCGTTATG 485
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1075 TGAAGCACTTTTTAATTTCTCATCAAGCAAGATCCAACTTTTCTAACTTTGTTAATG 1134
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 486 GAGTATGACACAGACATTTACCGGTTTTCAGCACTATATAGTTTCAACACGAGCG 545
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1135 AGATATGTCCTGAGTCAATCAACCGAATTAATTAACCACTACTATTAACACAGAGA 1194
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 546 ATGCTATCTTCTATGTCAAAATTTACACATACCAAAATCTTCAGAGCTTGGCTTATATC 605
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1195 ATGCTCTCATCTACGTGAAGCTGTATACATATCAATCTTCAGGGATAGCATATATC 1254
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 606 CATACTGCTCCTGGTGTGCTCCACAGAGATATAAAACCAAAATCTTTGTTGTTATCCC 665
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1255 CATACCGCTCGGAGTTTGCCATAGGGATGTAAGCCTCAAAATCTTTTGGTTCTATCCT 1314
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 666 CACACCATCAGTGAAGCTCTGATTTTGGAGTGCAAACTACTGTTGAAGGTGAA 725
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1315 CTACTCACCAGTTAAGCTATGTGATTTTGGAGTGCCAAAGTCTCTGGTCAAGGGTGAA 1374
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 726 CCAACATATCATATATCTCTCTCGGTATATACCGAGCTCCAGAACTCATCTTTTGGTCC 785
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1375 TCAACATTTTCATACATATGTTCAAGTTACTATCGGCTCCAGAACTAATATTTGGTGA 1434
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 786 ACAGAGTATACATCATCATGATATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 845
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1435 ACTGAATACACACCTTCTATTTGATATCTGTCAGCTGTTGTTGTTGTTGTTGTTGTTGTT 1494
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 846 CTTTGGGACCGGTTATTTCCCGGAGGAAATTTCTGTGACCACTAGTTGGAGATCATAAAG 905
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1495 CTAGGACAGCCATTTGTTTCTGGAGAAATCAGGTGACCAACTGTGTGGAATTTATTAAG 1554
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 906 GTTCTTGGTACTCCAACTCCGGAAGAAATCCGGTGCATGAACCCAACTACACAGACTTC 965
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1555 GTTCTTGGTACTCCGACTCCGGAGAAATCCGTTGCATGAACCCAACTATACAGATTTT 1614
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 966 AGATTCCCACAAAATCAAGCCACCTTTGGCATTAAGGTTTTCACAAGCGGATGCTCCG 1025
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1615 AGATTCCCTCAGATTAAGCTCATCTTTGGCACAAGGTTTTCACAAGCGAATGCTCTCT 1674
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY 1026 GAAGCAATTGACCTTGCATCTCGGCTTCTTCAATACTCACCAGTCTACGTTGCACCTGG 1085
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1675 GAAGCAATTGACCTTGCATCAAGGCTTCTCCAAATATTCACTAGTCTACGCTGCACCTGG 1734
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1086 CTCGAGGCATGTGCGCATCCGTTTTTCAATGAATCCCGTAGCCAAATGCTCGTCTTCCA 1145
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1735 CTGGAAGCATGTGCACATCTCTTTTGTATGAGTTCGCGAGCAAAATGCCGTTCTCTCT 1794
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1146 AATGCGCGACCTCTACCAACCGTTGTTCAACTTCAACAGAGGTTGTTCTGCGGCTTCACCG 1205
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1795 AATGCGCATTCCTACTGCCCACTTTTCAACTTCAACAGAGGTTAGCTGGAGCATCACCT 1854
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1206 GAGCTTATCAACAGGCTAATACAGAGCATGTGAGGCGACAGATGAATCGTGGCTTTCCA 1265
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1855 GAACCTGATCAATAGGCTCATCCAGAGCATATTAGCGGCAGATGGGTCTCAGCTTCCCG 1914
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1266 TTTCAAGCTGGACCTTAGA 1284
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1915 CATTCGCGGTTTCATAGA 1933
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
US-10-292-408-15
; Sequence 15, Application US/10292408
; Publication No. US20030182692A1
; GENERAL INFORMATION:
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: DA COSTA E SILVA, OSWALDO
; APPLICANT: CHEN, RUOYING
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METHODS
; FILE REFERENCE: 16313-0178
; CURRENT APPLICATION NUMBER: US/10/292,408
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/346,096
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 1621
; TYPE: DNA
; ORGANISM: Brassica napus
US-10-292-408-15

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Query Match
  43.3%; Score 709; DB 16; Length 1621;
Best Local Similarity 76.6%; Pred. No. 4.5e-129;
Matches 868; Conservative 0; Mismatches 265; Indels 0; Gaps 0;

QY 161 GTCTGCTGCTTTATAGAAAGGAAATGATGCTGTTACCGGTGCACATAATTTCTACTACAAT 220
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 155 GCGGCTGCTGTAGTTGATGGACATGACCAAGTCACTGGCCACATAATCTCCACCACCAT 214
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 221 TGAGGCAAAAATGGTGAACCTTAACAGACCATTTAGTTACATGGCCGAAGGTTGTTGG 280
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 215 CGGTGTAATAAACCGAGAACCAAAAACAGACAATAGTTTACATGGCGGAGCGAGTTGTCGG 274
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 281 AACAGATCATTCGGAATTTGATTTCCAGGCAAAATGCTTGGAACTGGAGAAATCAGTAGC 340
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 275 TACAGCTCTTTCGGGATAGTGTTCAGGCGAAGTGTCTGGAGACTGGAGAAACCGTGGC 334
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 341 CATTAAGAAGGTTTTCGAAGATCGCGTTTATAAAAAACCGAGAGTTGCAATTTAATGGGACT 400
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 335 GATAAGAAGGTTTTCGAAGACAGGAGGTACAAGAACCGAGAGCTTCAGCTGATGCTGT 394
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 401 AATGGAACCATCCAATGTGGTTTCTTTGAAGCATTTGTTCTTCTTACACGACTAGAGA 460
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 395 GATGGAACCATCCGAATGTTGTTTGAAGCATTTGTTCTTCTCGACCAACGAGCAAGA 454
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 461 TGAGCTTCTCCCAATCTCGTTATGAGTATGTPACAGAGACATTGTPACCGGTTTGA 520
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 455 CGAGCTGTTTCTGAACCTTGTTATGAGTATGTCCTTGAGAGCTTGACGAGTTCTGAA 514
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY 521 GCACTATAGTCTCAACACGAGGATGCTATCTTCTATGTCAAACTTTACACATACCA 580
Db 515 ACATTACAGCATGCTAAACAGAGGATGCGCTGTTTATGTAACTCTATATGTACCA 574
QY 581 AATCTTCAGAGGCTTGGCTTATATCATATCTCTCTGCTGTCTGCCACAGAGATATAA 640
Db 575 GATCTTCAGAGACTTGTCTTACATTCACAAATGTTGCTGGAGTTTGCACAGAGATCTAA 634
QY 641 ACACAAATCTTTTGGTTGATCCCAACCAATCAGTGTAAAGTCTGTGATTTTGGAG 700
Db 635 GCGTCAAAATCTTCTGTTGATCCTCTGACTCATCAAGTGAAGATCTGTGATTTTGGCAG 694
QY 701 TSCAAAGTACTGTTGAAGGTAACCAACATATATATATCTCTCTGCTGTATATACG 760
Db 695 TCGCAAAACAGCTTGTAAAGGTAAGCCAACTCTCTTACATATGTTCAAGATTTCTACCG 754
QY 761 AGCTCCAGAACTCATCTTTGGTGCCACAGATATATCATCATCATATGATGTCTGCTGC 820
Db 755 TGCACCTGAACTTATATTCGGTGCCACTGAGTACACAACTTCATTTGATTTGGTCTGC 814
QY 821 TGGTTGTTTCTGGCAGAGCTACTTCTTGGGAGCGGTTTATTCGGGGAGAAAAATTCGT 880
Db 815 TGGTTGTTTCTCGCTGAGCTTCTTCTTGGTCAAGCACTATTCCTTGGAGAAAAATGCTGT 874
QY 881 GACACAGCTAGTGGAGATCATAAAGTCTTCTGCTACTCCAACTCGGGAAGAAATCGGTG 940
Db 875 GGGTCAGCTCGTTGAAATCATCAAAATCTTGGTACCAAACTCGAGAAAGATCCGTTG 934
QY 941 CATGAACCCAACTACACAGACTTCAGATTTCCCAAAATCAAGCCCACTTGGCATAA 1000
Db 935 TATGAATCCCACTACACAGACTTTAGTTCCCGAGATTAAGGACATCTCTTGGCAACA 994
QY 1001 GGTATTTCCAACAGCGGATGCTCCGGAAGCCATTGACCTTGGCATCTCGGCTTCTTCAATA 1060
Db 995 GATTTTCCAACAAAGATGCTCCGAGAGCCATTGATTTGTCATCAAGGCTCTTCACTA 1054
QY 1061 CTCACAACTAGTGTGACATCGGCTCGAGGATGTTGGGATCGGTTTCAATGAAC 1120
Db 1055 CTCCTCAAGTCTTAGATGACAGCGCTTGAAGCTTGTGACATCGGCTTCTTGTGATGAGCT 1114
QY 1121 CCGTGAGCCAAATGCTGCTTCCAAATGGCGGAGCTCTPACCACGCTTGTTCACCTCAA 1180
Db 1115 TAGAAGACCAAAATGCTGTTTACCAAAACGAGCGGCTTTCGGCGGCTCTTCAACTCAA 1174
QY 1181 ACAAGAGTTGTCTGGGGCTTCCCGGAGCTTATCAACAGGCTAATACAGAGCATGTGAG 1240
Db 1175 ACAAGAGGTAGCTGGAGCTTCACTGAGCTGCTCAACAGTTGATTCAGACCATATCA 1234
QY 1241 GCGACAGATGAATGGTGGCTTTCATTTCAAGCTGAGCCCTAGAAAAGGATC 1293
Db 1235 GACGAGTTGGGTCTAAGCTTCTTGAATCAGTCTGGAACCTTAAACAAACGATC 1287

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RESULT 8

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US-10-424-599-67987
; Sequence 67987, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 67987
; LENGTH: 1881
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:

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; OTHER INFORMATION: Clone ID: PAT_MRT3847_32405C.1
US-10-424-599-67987
Query Match 43.3%; Score 708.6; DB 18; Length 1881;
Best Local Similarity 76.7%; Pred. No. 5,8e-129;
Matches 867; Conservative 0; Mismatches 264; Indels 0; Gaps 0;
QY 120 TCTTTGAAACGTGCTCCGATATAGAACAGCAAGGAAATGTCTGTCTGCTGTATAGAA 179
Db 113 TCTCTCTCTCTCCCTCCGATGCTGAGGATAAGGAGATGCTACCTCTCTGTCAAT 172
QY 180 GGAATGATGCTGTCTACCGGTACATAATTTCTACTACAATTTGGAGGCAAAATCGTGA 239
Db 173 GGAATGATTCCTTAACCTGGAACATCATATCTACACTATTTGGAGGCAAAATGGGAA 232
QY 240 CCTAAACAGACCATTTAGTTTACATGGCCGAACGTGTTGTTGGAAACAGGATCATTCGGAAT 299
Db 233 CCCAAACAGACTTTTAGTTTACATGGCAGAACGGGTTGTAGGAACCTGGATCATTTGGAAT 292
QY 300 GTATTCAGGCAAAATGCTTGGAAACCTGGAATCAGTAGCCATTAAGAGGTTTTCGAA 359
Db 293 GTTTTCCAGGCAAAATGCTTGGAAACCTGGGAGGAGTGGCAATTTAAAAGGTTTTCACAA 352
QY 360 GATCGCCGTTTAAAAACCGGAGAGTTGCAATTTAATGGCACTAATGGACCATCCAATGTG 419
Db 353 GACAGAAGATCAAGAATCGTGAACCTACAGTTAATGCGTGTGATGATCATCCAAATGTG 412
QY 420 GTTCTCTTGAAGCATTTGTTCTTCTCAACAGACTAGAGATGAGCTCTTCTCAATCTC 479
Db 413 ATCTCTTGAAGCATTTGTTCTTCTCACTACAGTACTGATGAATTTTCTTAATTTG 472
QY 480 GTTATGGAGTATGTACACAGAGACATTTGACCGGGTTTTGAAAGCACTATATACTAGTTCAAAC 539
Db 473 GTGATGGAGTATGTTCAGAGTCCATGTATAGAGTCTTTAAAGCACTACAGCAATGCTAAT 532
QY 540 CAGCGGATGCTCTTCTTCTTCAAACTTTTACATATACCAATCTTTCAGAGGCTTGGCT 599
Db 533 CAAAGAATGCTCTATCATCTACGTTTAAACTTTATATGTACCAAGATTTTCAGGGGGTGGCT 592
QY 600 TATATCCATATCTGCTCTGCTGTCTGCCACAGAGATATAAAACCAACAAATCTTTTGGTT 659
Db 593 TATATCCACATCTGTTCCCAAGTTTGCACAGAGATTTGAAAGCTCAAAATATATCTGTTG 652
QY 660 GATCCCCACCCATCAGTGTAAAGCTCTGTGATTTTGGAAAGTGCAAAAGTACTGTGTA 719
Db 653 GATCTCTTTACACACCAAGTGAAGCTATGTGACTTTTGAAGTGCAAAAGTCTTAGTCAA 712
QY 720 GGTGAACCAACATATCATATATCTGCTCTCGGTATTTACCGAGCTCCAGAACTCATCTT 779
Db 713 GGTGAAGCTAATATATCATATATGTTTACCGGTTCTATCGAGGACCAAGACTCATATTT 772
QY 780 GGTGCCACAGAGTATACATCATCTCAATTCATATATGCTGTCTGCTGTGTTGTTCTGCGCAG 839
Db 773 GGGGCCACAGAGTATACAGTTCAATGATATTTGGTCAGCTGGCTGTGCTCTGCTGNA 832
QY 840 CTACTCTTTGGGAGCGGCTTATTTCCCGGAGAGAAATTTCTGGACAGCTAGTGAGATC 899
Db 833 CTCTTTTGGGCGCAGCCATTTATTCCTGCGCAAAATGCAAGTAGACCACTGTGATCAAT 892
QY 900 ATAAAGTTTCTTGGTATCTCCAACTCGCGCAAGAAATCCCGTGCATGAACCCAACTACACA 959
Db 893 ATAAAGGTGCTTGGCAGCCCACTCGAGAGGAAGTACGCTGTATGAATCCCAATTTACAA 952
QY 960 GACTTCAGATTTCCCAAAATCAAGCCCACTCGGCTTGGCAATAAGTTTCCCAAGCGGATG 1019
Db 953 GACTTTAGGTTTCTCAGATAAAAGCACACCCATCGCAAGATATTCACAAAAAGATG 1012
QY 1020 CCTCGGAAGCAATGACCTTGCATCTCGGCTTCTTCAATATCTCACCAAGCTACGTGTC 1079
Db 1013 CCTCGGAAGCTATTTGATCTTGGCATCCCGGCTTGTGCAATCTCCCAAGTCTCCGGTGC 1072
QY 1080 ACTGCGCTCGAGGATGTCGATCCGTTTTCATATGAATCCCGTGGAGCAAAATGCTGCT 1139

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Db 1073 ACTGCATTGAAGCATGTGCACATCCTTTCTTTGATCAACTTCGTGAAACCAACGCTCGC 1132
Qy 1140 CTTCCAAATGGCGAGCTCTACACCGTTGTTCAACTTCAAAAGAGTTGCTGGGCT 1199
Db 1133 CTGCCAAATGGTCGCCAATTCCTCCCTCTATTTAACTTCAACAGGAATATCTGGAGCA 1192
Qy 1200 TCACCGGAGCTTATCAACAGGCTTAATACAGAGCATGTGAGGCGACAGATG 1250
Db 1193 TCTCCGAGCTTCTTAATAGTTGATACCTGACCATTGTGAGCGGCAATG 1243

RESULT 9
US-10-425-114-12807
; Sequence 12807, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 12807
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701212714_FLI
US-10-425-114-12807

Query Match 43.2%; Score 707; DB 18; Length 1726;
Best Local Similarity 76.6%; Pred. No. 1.1e-128;
Matches 866; Conservative 0; Mismatches 265; Indels 0; Gaps 0;

Qy 120 TCTTTGAAACGTCGTCCGATATAGACAACGACAGAAATGCTGCTGTATTAGAA 179
Db 71 TCTCTCTCTCTCCCTCCGCTAGGCTGAGGATAGGAGATGCTACCTCTGTCAAT 130
Qy 180 GGAATATGTCCTGTACCGCTACATAATTTCTACTACAAATCGAGGCAAAATGTGAA 239
Db 131 GGAATATGTCCTGTACCTGTGTACATATCTACAACTATTGGAGCAAAATGGGAA 190
Qy 240 CCTAAACAGACCATATTAGTTACATGCGCGAAACGTTGTTGGAAACAGGATCATTCGGAAT 299
Db 191 CCCAAACAGACTATTAGCTACATGCGCAGAACGGGTTGTAGAACTGGATCATTTGGAATC 250
Qy 300 GTATTCAGGCAAAATGCTTGGAAACCTGGAGAACTAGTAGCCATTAAGAAAGTTTGGCAA 359
Db 251 GTTTTCCAGGCAAAATGCTTGGAAACCTGGGAGGAGCTGGCAATTAAGAAAGTTTACAA 310
Qy 360 GATCGCGCTTATAAAGACAGAGTTGCAATTAATGCACTAATGACCAATCCAAATGTG 419
Db 311 GACAGAAGATACAGAATGTCGAATGTCAGTTAATGCGTGTGATGATCAATCAATGTG 370
Qy 420 GTTTCTCTTGAAGCATTTGTTCTTCTCAACAGCATAGAGATGAGCTCTTCTCAATCTC 479
Db 371 ATCTTTTGAAGCATTTGTTCTTCTCAACATCAAGTACAGATGAACTTTTCTCAATTTG 430
Qy 480 GTTATGAGATATGTACAGAGACATTTGACCGGTTTGAAGCACTATATAGTTCAAAAC 539
Db 431 GTGATGAGATATGTTCACAGAGTCCATGTATAGAGTCTTAAAGCACTATAGCAATGTCAAT 490
Qy 540 CAGGAGATGCTATCTCTATGTCAAACTTTTACATACCAATCTTCAGAGCTGGCT 599
Db 491 CAAAGAAATGCAATCATCTACGTAAACCTTTATATGTACAGATTTTCAGGGGGTGGCT 550
Qy 600 TATATCCATAGTCTCTGCTGTGTCTGCCACAGAGATATAAAACCAAAATCTTTTGGTT 659
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Db 551 TACATCCACACTGGTCCCAAGTTTGGCCACAGAGATTTGAAGCCTCAAAATATATCTGGTG 610
Qy 660 GATCCCCACACCCATCAGTGTAAAGCTCTGTGATTTTGGAGTGCAAAAGTACTGGTGA 719
Db 611 GATCTCTTTACACACCAAGTGAAGCTATGTGATTTTGGAAAGTGCAAAAGTTCTAGTCGAA 670
Qy 720 GGTGAACCAAAACATATCATATATCTGCTCTCGGTATTTACCGAGCTCCAGAACTCATCTTT 779
Db 671 GGTGAAGCTTATATATCATATATGTTTCAAGTTCTATCGAGCACCAGAACTTATATTT 730
Qy 780 GGTGCCACAGATATACATCATCATCATATGATATGTTGCTGTGTTGTTGTTCTGGCAGAG 839
Db 731 GGGGCCACACAGATATACAGATTCGATGATATTTGGTCAGCTGGCTGTGTTCTTGTCTGAA 790
Qy 840 CTACTTCTTGGCGAGCGCTTATTCGGGAGAAATTTCTGTGACACAGCTAGTGGAGATC 899
Db 791 CTTCTTTTGGGCGAGCCATTATTTCCCTGGCGAAAATGCAAGTACAGCAGCTTGTACATAT 850
Qy 900 ATAAAGGTTCTTTGGTACTCCTCAACTCGCGAAGAAATCCGGTGCATGAACCAAACTACACA 959
Db 851 ATAAAGTCTTTGGGACACCCACCCGAGAGGAGTACGCTGTATGATCCCAATTACAAT 910
Qy 960 GACTTCAGATTTCCCAAAATCAAAAGCCACCTTGGCATPAAGGTTTTCACAAGCGGATG 1019
Db 911 GACTTTAGGTTTCCACAGATAAAAGCACACCCTACAGATATTCACAAAAAGATG 970
Qy 1020 CTTCCGGAAGCATTGAACCTTGCATCTCGGCTTCTTCATATCTCACAAGTCTACGTTGC 1079
Db 971 CTTCCAGAAAGCTATTGATCTTGCATCTCCCGCTTTTGCATATCTCCCAAGTCTCCGGTGC 1030
Qy 1080 ACTGCGCTCGAGCATGTCGCATCGTTTTCATATGAATCCGTGAGCAAAATGCTCGT 1139
Db 1031 ACTGCGCTTGAAGCATGTGCATCTCTTCTTTGATGAACCTTCGTAACCTATGCTCGC 1090
Qy 1140 CTTCCAAATGGCGACCTCTACACCGTTTGTTCAACTTCAAAACAGAGTTGTCTGGGCT 1199
Db 1091 TTGCCAAATGGTGTGCTCAATTTCCCTCTATTTAACTTCAACAGGAATATCTCGAGCA 1150
Qy 1200 TCACCGGAGCTTATCAACAGGCTTATACAGAGCATGTGAGGCGACAGATG 1250
Db 1151 TCTTCGAGCTTGTTAATAAGTTGATACCTGACCATGTGAAGCGCAAAATG 1201

RESULT 10
US-10-424-599-67990
; Sequence 67990, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 67990
; LENGTH: 1979
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_32408C.1
US-10-424-599-67990

Query Match 43.2%; Score 707; DB 18; Length 1979;
Best Local Similarity 76.6%; Pred. No. 1.2e-128;
Matches 866; Conservative 0; Mismatches 265; Indels 0; Gaps 0;

Qy 120 TCTTTGAAACGTCGTCCGATATAGACAACGAGAAATGCTGCTGTATTAGAA 179
```

Db 289 TCTCTCTCTCCCTCCGCTGCTGAGGATAAGGAGATGCTTACCTCTGTCTCATCAAT 348
QY 180 GGAATATGCTGTACCGGTACATATTTCTACTACAAATTTGGAGGCAAAATGGTGA 239
Db 349 GGGAAATGATTCCTTAACCTGCTACATCATATCTACAACCTATTTGGAGGCAAAATGGGAA 408
QY 240 CTTAAACAGACATTTAGTTTACATGCGCAACCTGTTTGGAAACAGGATCATTCGGAAAT 299
Db 409 CCCAAACAGACTTTAGCTTACATGGCAGAACCGGTTGTAGGAACCTGGATCATTTGGAATC 468
QY 300 GTATTCCAGGCAAAATGCTTGGAACTGGAGAAATCAGTAGCCATTAAGAAGGTTTGGCAA 359
Db 469 GTTTTCCAGGCAAAATGCTTGGAACTGGAGGAGGAGTGGCAATTTAAAGGTTTACAA 528
QY 360 GATCGCGTTATAAAACCGAGAGTTGCAATTAATGCGACTAATGAGCAATCAAAATGTG 419
Db 529 GACAGAAGATACAAGAAATCGTGAACCTGCAAGTAAATGCGTGTGATGATCATCAAAATGTG 588
QY 420 GTTTCCTTGAAGCATTTGTTCTCTCAACGACTAGAGATGAGCTCTTCTCAATCTC 479
Db 589 ATCTCTTTGAAGCATTTGTTCTCTCAACCTACAAGTACAGATGAACCTTTTCTCAATTTG 648
QY 480 GTTATGGAGTGTACCCAGAGACATTTGACCGGGTTTGAAGCACTATATACTAGTTCAAA 539
Db 649 GTGATGGAGTATGTTCCAGAGTCCATGTATAGTCTTAAAGCACTATAGCAATGCTAAT 708
QY 540 CAGCGGATGCTTATCTTCTATGCTAACTTTACATACCAAAATCTTCAGAGGCTTGGCT 599
Db 709 CAAAGAAATGCCAATCATCTACCTAAACCTTTATATGTACCAAGATTTTCAGGGGGTTGGCT 768
QY 600 TATATCCACTGCTCTGCTGCTGCCACAGATATAAACCACAAATCTTTTGGTT 659
Db 769 TACATCCACTGGTCCAAAGTTTGGCCACAGAAATTTGAAGCCCTCAAAATATATCTGGTG 828
QY 660 GATCCCCACACCCATCAGTGTAAAGTCTGTGATTTTGGAAAGTGCAAAAGTACTGGTGAA 719
Db 829 GATCTCTTACACACCAAGTGAAGTATGTGATTTTGGAAAGTGCAAAAGTACTGGTGAA 888
QY 720 GGTGAACCAACATATCATATATCTGCTCTCGGTATTAACGAGTCCAGAACTCATTTT 779
Db 889 GGTGAAGCTAATATATCATATATGTTTCAAGTCTTCAAGTCTTCAAGTCTTCAATTT 948
QY 780 GGTGCCACAGATATACATCATCATATGATATATGCTGCTGCTGCTGCTGCTGCTGCTG 839
Db 949 GGGGCCACAGAGTATACAGATTCGATGATTTTGGTCAAGTCTGCTGCTGCTGCTGCTG 1008
QY 840 CTACTTCTTGGCAGCGTATTTCCGGGAGAAATTTCTGCGAGCAAGTCTAGTGAGATC 899
Db 1009 CTTCTTTTGGCCAGCCATTTATCTCTGCGAAATGCAAGTAGACCAAGTCTGATATTT 1069
QY 900 ATAAAGGTTCTTGGTACTCCAACTCGCAAGAAATCCCGTGCATGAACCCCAAACTACACA 959
Db 1069 ATAAAGGTTCTTGGCAGACACCCACCGGAGGAAGTACGCTGTATGAATCCCAATTTACA 1128
QY 960 GACTTCAGATTTCCCAAAATCAAAGCCACCTTGGCATTAAGTTTTCAGAGCGGATG 1019
Db 1129 GACTTTAGGTTTCCACAGATAAAGCACACCCATGGCACAAGATATCCACAAAAGATG 1188
QY 1020 CTTCCGGAAGCATTTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1079
Db 1189 CTTCCAGAAAGCTTTGATCTTGCATCCCGCTTTTGGCAATATCTCCCAAGTCTCCGGTGC 1248
QY 1080 ACTGGGCTCGAGGCAATGTGCGATCCGTTTTCATGAATCCGTTGAGCAAAATGCTCGT 1139
Db 1249 ACTGGCTTGAAGCATGTGCATCTTTTGTGATGAATCTCGTGAACCTTAATGCTCGC 1308
QY 1140 CTTCAAAATGGCCGACTCTACACCGTTTTCATCTTCAAAACAGAGTTGTCTGGGGCT 1199
Db 1309 TTGCCAAATGGTGTCTCAATTTCCCTCTATTTAACTTCAAAACAGGAATTTCTGGAGCA 1368
QY 1200 TCACCGGAGCTTTATCAACAGGCTATATACAGAGCATGTGAGCGGACAGATG 1250
Db 1369 TCTTCCGAGCTTGTTAATAAGTTGTATCCTGACCAATGTGAAGCGGCAAAATG 1419

RESULT 11

US-10-292-408-21
; Sequence 21, Application US/10292408
; Publication No. US20030182692A1
; GENERAL INFORMATION:
; APPLICANT: VAN THIELEN, NOCHA
; APPLICANT: DA COSTA E SILVA, OSWALDO
; APPLICANT: CHEN, RUOYING
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METHODS
; FILE REFERENCE: 16313-0178
; CURRENT APPLICATION NUMBER: US/10/292,408
; PRIOR FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/346,096
; FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 1499
; TYPE: DNA
; ORGANISM: Glycine max
US-10-292-408-21

Query Match 43.1%; Score 705; DB 16; Length 1499;

Best Local Similarity 77.1%; Pred. No. 2.7e-128;

Matches 858; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

QY 136 CCGATATAGACACGACAAAGGAAATGCTGCTGCTGTTATAGAGGAATGATGCTGTA 195
Db 159 CCGACCGCGGACCGAAAGGAATGTGAGTCTGTCGAGATGTAATGATGACTCA 218
QY 196 CCGGTACATAATTTCTACTACAAATTTGAGGCAAAATGTTGAACCTAAACAGACATTA 255
Db 219 CTGGTACATAATCTCAACCAATTTGAGGCAAAATGTTGAACCTAAACAGACATCA 278
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Db 279 GTTACATGCGCAAGCTGTTGTTGCACTGATCATTTGGCATTTGTTTCCAGGCGAAGT 338
QY 316 GCTTGGAACTGGAGAACTAGTACCAATTAAGAGGTTTTCGCAAGATCGCGTTATAAAA 375
Db 339 GCTTGGAGACTGGCGAGGACGATGCTATAAAGAGTCTTGCGAGACAGGCGGATACAAA 398
QY 376 ACCGAGAGTTCCAATTAATGCGACTTAATGAGCACTTCCAAATGTTGTTTCTTGAAGCAT 435
Db 399 ATCGTGAAGTCAATTAATGCGGATGATGATCAACCAATATATTTCTTGAAGTACT 458
QY 436 GTTCTTCTTACAAACGACTAGAGATGAGCTCTTCTCAATCTCGTTATGAGATGATAC 495
Db 459 ATTTCTTCTTACAAACGACTAGAGATGAGCTTTTCTGAACTTGGTATGGAATATGTC 518
QY 496 CAGAGACATTTGACCGGTTTGAAGCACTATAGTTCAACCGCGGATGCTCTATCT 555
Db 519 CTGAGACGATCTTCGTTTATAAGCACTACAGTAGCATGAACAGAGAAATGCCCCATA 578
QY 556 TCTATGTCAAACTTTTACACATACCAAACTTTTCAAGGCTTGGCTTATATCCATATGCTC 615
Db 579 TCTATGTGAATATATACATATCAATCTTTAGGGAGTGGCGTATATCCATATGATAC 638
QY 616 CTGGTGTCTGCCACAGAGATATAAAACCAAAATCTTTTGGTTGATCCCCACACCCATC 675
Db 639 CAGGAATCTGCCATAGGATTTGAAGCCTCAAAATCTTTTGGTTGATCGACTCACACACC 698
QY 676 AGTGTAACTCTGTGATTTTGAAGTGAAGTACTGGTGAAGGTGAACCAAAATATAT 735
Db 699 AAGTCAAGCTCTGTGATTTTGGAGTGAAGTCTCAAAATCTTTTGGTTGATCGACTCACACACC 758
QY 736 CATATATCTGCTCTCGGTATTAACCGAGCTCCAGAACTCATCTTTGGTCCACAGAGTATA 795
Db 759 CATACATATGTTCAAGTACTATCTGTCGCCACAGACTAATATTTGGTGGCGGAGATACA 818

APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
NUMBER OF SEQ ID NOS: 204966
SEQUENCE ID NO: 29872
LENGTH: 1922
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_34331C.1
US-10-437-963-29872

Query Match 42.4%; Score 694.2; DB 19; Length 1922;
Best Local Similarity 77.6%; Pred. No. 3.9e-126; Mismatches 243; Indels 0; Gaps 0;
Matches 840; Conservative 0; Mismatches 243; Indels 0; Gaps 0;

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DB |||||
QY 1703 TGCTTCTCTTATGGAAGGAGTGTCTGTACCGGCCACATAATCTCCAGCAAGTTGG 1644
DB |||||
QY 224 AGGCAAAATGCTGAACCTTAACAGACCATTTAGTTACATGCGCGAAGCTGTTTGGAAAC 283
DB |||||
QY 1643 AGGGAAGAAATGAGAACTTAAGGAGCATTTAGTTACATGCGCAGAACGAGTTGTGGGAAC 1584
DB |||||
QY 284 AGGATCATTCGAATGATTTCCAGGCAAAATGCTTGGAACTGAGAAATCAGTAGCCAT 343
DB |||||
QY 1593 TGGATCATTTGGAATCGTCTTTTCAGGCAAAATGTTTGGAGACTGTGTGAGCTGTCGCCAT 1524
DB |||||
QY 344 TAAGAAGGTTTTCAGAGTGCCTGTTATATAAAGCGAGGTTGCAATTAATTCGCACTAAT 403
DB |||||
QY 1523 TAAGAAGGTTTACAGCAACGTTTACAGCAAGGAGTTGCAATTAATTCGCACTAAT 1464
DB |||||
QY 404 GGACCATCAAAATGCTGTTTCTTGAAGCAATTTCTTCTTCTACAGCACTAGAGATGA 463
DB |||||
QY 1463 GGATCATTCGAATGTTTCTTGAAGCAATTTCTTCTTCTACAGCACTAGAGATGA 1404
DB |||||
QY 464 GCTCTTCTCAATCTGTTAGTAGTAGTACAGAGACATTTGACCGGTTTGAAGCA 523
DB |||||
QY 1403 ACTTTTCTTAACTCGTGTGATGAAATTTGTTCTGAGTCACTGTATCGTGTGTTGAAGCA 1344
DB |||||
QY 524 CTATACTAGTTCAACACGAGGATGCTATCTTCTATGTCAAACTTTACACATACCAAT 583
DB |||||
QY 1343 TTATAGCAACATGAACCAAGGATGCCACTTATATATGTCAATTTGATGTTTACAGAT 1284
DB |||||
QY 584 CTTACAGAGCTTGGCTTATATCATATCTGCTCTGCTGCTGCTGCCACAGAGATATATAAAC 643
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DB |||||
QY 764 TCCAGAACTCATCTTTTGGTGCACAGATATATCATCTCATTTGATATATGCTGCTGCTGG 823
DB |||||
QY 1103 TCCAGAACTGATTTTGGGCAACCGAATACAGCACTCAATTTGATATATGTTGCTGCTGG 1044
DB |||||
QY 824 TTGTTCTTGGCAGAGTACTTTCTTGGCAGCCGTTATTTCCGGGAGAAATTTCTGTGGA 883
DB |||||
QY 1043 GTGTGTTCTGTGAGTTGCTCTCTTGGCCAGGCTCTCTTCTGTTGAAAGTGCAGTGA 984
DB |||||
QY 884 CCAGCTAGTGGAGATCATAAAGGTTCTTGGTACTCCAACTCCGCAAGAAATCCGCTGCAT 943
DB |||||
QY 983 TCAGCTTGTGAGATTAATAAGGTTCTTGGTACTCCAAACAGTGAAGGAAATCCCGCTGCAT 924
DB |||||

RESULT 14

US-10-437-963-98579/c
; Sequence 98579, Application US/10437963
; Publication No, US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 98579
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96473C.1
US-10-437-963-98579

Query Match 42.2%; Score 689.8; DB 19; Length 1831;

Best Local Similarity 78.1%; Pred. No. 2.8e-125;

Matches 829; Conservative 0; Mismatches 232; Indels 0; Gaps 0;

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DB |||||
QY 1591 GACGCGTGACGGTTCACATCTCCACCACTTCGCGCGCAAGACGGCGAGCGGAG 1532
DB |||||
QY 246 CAGACCAATAGTTACATGCGCGAAGCTGTTGTTGGAACAGGATCATTCGGAATTTGATTC 305
DB |||||
QY 1531 CGGCAATTAGTTATATGCGCGAGGAGTTGTTAGGAATGTTCTTCGGGATTTGTTTC 1472
DB |||||
QY 306 CAGGCAAAATCCTTGGAAATCTGGAGAACTAGTACCATTAAGAGGTTTTCGAAGATCGC 365
DB |||||
QY 1471 CAGGCTAAGTCTTGGAGACGGGGGAAACCGTGGCCATCAAGAGGTTTTCAGGACCGG 1412
DB |||||
QY 366 CGTTATAAAACCGGAGGTTGCAATTAATGAGTCTTAATGGACCATCCAAATGTGTTTCC 425
DB |||||
QY 1411 GCTTACAGAACCGGTGAACCTGAGCTTATGCGCAATGGAAACACCCCAATGTCATGTC 1352
DB |||||

Qy	426	TTGAAGCATGTGTTCTTCTCTCTA	CAA	CGACATAGAGATGAGCTCTCTCCATCTCGTTATG	485
Db	1351	CTGAAGCACATGCTTCTTCTCTCA	CCAA	CGACAGGAGATGAGCTGTTCCTGAAATCTTGTTATG	1292
Qy	486	GAGTATGTACCAGAGACATGTG	ACCGGGTTTTGA	GCACATATCTAGTCTCAAACACGCGG	545
Db	1291	GAGTACGTCCCTGAGACACTCT	ACCGTGTGCTCA	AGCACTTACGCAATGCTAACCGCGG	1232
Qy	546	ATGCCTATCTTCTATGTCAA	ACTTTTACA	CATPACCAAAATCTTTCAGAGCTTTGGCTTTATATC	605
Db	1231	ATGCCAATTGATCTATGTGA	AGCTTTACATCTAT	CAGCTTTTCAGAGGTTAGCTTATATT	1172
Qy	606	CATACTGCTCCTGTGTCTGCC	ACAGAGATATAAA	CCACAAATCTTTTGGTTGATCCC	665
Db	1171	CATACTGTTCCAGAGTCTGCC	ACAGGATGTGAA	CCACAAATGTTTTTGGTTGATCCT	1112
Qy	666	CACACCATCAGTGTAA	AGCTCTGTGATTTTGGAA	AGTGCAAAAGTACTGTGTGAAAGTGAA	725
Db	1111	CTCACTCATCAAGTCA	AGCTATGTGACTTTGGAA	GTGCNAAGTTCTGTGTTCCGTGGTGAA	1052
Qy	726	CCAAACATATCATATATCTG	CTCTCGGTATTA	CCGAGCTCCAGAACTCATCTTTGTGTGCC	785
Db	1051	CCGAACATATCATACATTTG	CTCTCGCTATTAT	CGTCTCCAGCTCATATTTGTGTGCA	992
Qy	786	ACAGATATACATCATCATTT	GATATATGTTGTTCTG	CTGTTCTTGGCGAGACTACTT	845
Db	991	ACCGAGTATACAACCTTCA	ATTGACATATGTGTCA	GCTGCGTTCTTGACAGATTACTT	932
Qy	846	CTTGGCGAGCCGTTTATT	CCCCGGGAGAAAATTTCT	GTGGACCAAGCTAGTGGAGATCATAAAG	905
Db	931	CTTGGTCAGCCACTGTTT	CTCTGGAGAGAGTGCTGT	TGCACCACTAGTAGAGATAATCAAG	872
Qy	906	GTTCTTGGTACTCCAACT	TCGGGAGAAAATTCGG	TGTGCATGAAACCCAACTACAGACTTC	965
Db	871	GTTCTTGGTACTCCAA	CCCGTGGAGAAAATACGA	TGTCATGAAACCCCAACTACTACTGAGTTC	812
Qy	966	AGATTCCCACAAATCAA	AGGCCCA	CCCTTGGCATTAAGGTTTTTCCACAAAGCGATGCCCTCCG	1025
Db	811	AAATTTCTCAGATTAG	GGCTCATCTCTTGGCA	CAAGAATTTTCCACAGAGAAATGCCCTCCA	752
Qy	1026	GAAGCCATTGACCTTGC	ATCTCGGCTTCTTCCAA	TACTCAACAAAGTCTACGTTGCATGCG	1085
Db	751	GAAGCCATAGACCTTG	CTTCTCCGCTCTTCTCCAA	TATTCACCAAGTCTACGCTGCACCTGCT	692
Qy	1086	CTCGAGCATGTGCGCAT	CCGTTTTTCAATGAA	CTCCGTGAGCCAAATGCTCGTCTTCCA	1145
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Qy	1206	GAGCTTATCAA	CAGGCTTAATAC	CAGAGCATGTGAGGGGACA	1246
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RESULT 15

US-10-424-599-67989
; Sequence 67989, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 67989

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Qy	1096	GTGCGCATCCGTTTTCATGAACTCCGTGAGCCAAATGCTGCTTTCCAAATGGCCGAC	1155
Db	1076	GTGCACATCCTTTCTTTGATGAACCTTCGAGAACCCCAATGCTGCGCTGCCAAATGGTCGTC	1135
Qy	1156	CTCTACCAACGTTGTTTCAACTTCAACAAGAGTTGCTGGGGCTTCACCGGAGCTTATCA	1215
Db	1136	CATTTCTCCTTTATTTAACTTCAAGCAGGAATTATCCGAAGCTTCTCCAGAGCTTGTGA	1195
Qy	1216	ACAGGCTAATACCAAGAGCATGTGAGCGGACAGATGAATGGTGGCTTTCATTTCAAGCTG	1275
Db	1196	ACAAAGTGATACCTGACCAACATGACGCGGCAATAGGGCTGCAATTTGTTCTCGCCGAC	1255
Qy	1276	GACCCCT	1281
Db	1256	GATCAT	1261

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 Job time : 1766.93 secs

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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 10:16:02 ; Search time 8124.57 Seconds
(without alignments)
7664.793 Million cell updates/sec

Title: X94938
Perfect score: 1636
Sequence: 1 TTTACTCTTCAGTCAGAGA.....AAAAAAAAAAAAAAAAAAAA 1636

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_hic:*
- 4: gb_est3:*
- 5: gb_est4:*
- 6: gb_est5:*
- 7: gb_est6:*
- 8: gb_gsa1:*
- 9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	949.4	58.0	1409	3	CNS0ABFT
2	949.4	58.0	1461	3	CNS0AB1V
3	704.8	43.1	709	1	AV782577
4	689.8	42.2	1197	9	CL957492
5	684	41.8	1745	3	AY106255
6	680.4	41.6	684	5	BP560588
7	673.2	41.1	690	1	AV782869
8	660.2	40.4	683	5	BP560678
9	654.6	40.0	1666	3	AY104068
10	620	37.9	558	1	AV822185
11	615	37.6	924	7	CK266410
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20	562.4	34.4	829	6	CB971865
21	560	34.2	1604	3	CNS0A4PT
22	558.8	34.2	1752	3	AY108486
23	548	33.5	963	7	CK286429
24	546	33.4	666	6	CD824216

25	546	33.4	821	6	CB894470	CB894470	EST647262
26	544.4	33.3	952	7	CK289285	CK289285	EST752007
27	542.2	33.1	944	7	CK290066	CK290066	EST752788
28	538.4	32.9	1870	3	CNS0ADOL	CD513745	Arabidops
29	538	32.9	887	6	CD574542	CD574542	UCRPT01_0
30	537.8	32.9	2036	3	CNS0A425	BX826501	Arabidops
31	533.8	32.6	876	7	CF208184	CF208184	CAB20003
32	529.4	32.4	1667	3	CNS0A5F6	BX823376	Arabidops
33	529	32.3	936	1	AV531495	AV531495	AV531495
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35	526.2	32.2	727	6	CD815282	BN15_02SM	CD815282
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41	507.2	31.0	910	7	CK273024	CK273024	EST719102
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45	502.4	30.7	934	7	CK266742	CK266742	EST712820

ALIGNMENTS

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LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSURLS12G09 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).
DEFINITION
ACCESSION BX815323.1 GI:42471412
VERSION
KEYWORDS HTG; GSLT cDNA
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE
AUTHORS Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1409)
GENOSCOPE
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis. Location/Qualifiers
1. 1409
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Col-0"
/db_xref="taxon:3702"

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Db	976	ACAAGGTTTTTTCATAAAGCGGATGCTCCAGAAGCAATAGACCTTTGCATCTCGGCTTCTTC	1035
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Db	1036	AATATTACCAAGTCTAGCTGCATCGCTCGAGCATGTGCTCATCGCTTTTCAATG	1095
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Db	1096	AACTCCGAGAGCAAAACGCCGCTTTCCAAATGGTCTGTCATTACCGCATTTGTTCAATT	1155
QY	1177	TCAAACAAGAGTTGCTTGGGGCTTCACCGAGCTTATCAACAGGCTAATAACAGAGCATG	1236
Db	1156	TCAAACAAGAGTTAGTGGAGCTTCAATGGAGCTAATCAACAGGCTAATACCTGAGCATG	1215
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Db	1216	TGAGACGCAAAATGAGCACAGGATTACAA	1244
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CNS0AB1V		1461 bp	mRNA
LOCUS	Arabidopsis thaliana Full-length cDNA Complete sequence from clone		
DEFINITION	GSLTSL42C04 of Silique of strain col-0 of Arabidopsis thaliana (thale cress).		
ACCESSION	BX817800		
VERSION	BX817800.1 GI:42471112		
KEYWORDS	HTC; GSLT cDNA.		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE	1 (bases 1 to 1461)		
AUTHORS	Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.		
TITLE	Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1461)		
AUTHORS	Genoscope.		
JOURNAL	Direct Submission		
COMMENT	Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr) - Web : www.genoscope.cns.fr) The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.		
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Qy      1029  GCCATTGACCTTGCATCTCGGCTTCTTCAATATCTACCAAGTCTACCTTGCACCTGCGCTC 1088
Db      1015  GCATAGACCTTGCATCTCGGCTTCTTCAATATTCACCAAGTCTACCGTGCACCTGCGCTC 1074
Qy      1089  GAGCGATGTCGGCATCCGTTTTCATATGAATCGTGTAGCGCAAAATGCTGCTTTCCAAAT 1148
Db      1075  GAAGCATGTGCTCATTCGGTTTTCATATGAATCGGATCCGAGAGCAAAACGCCCTCTTCCAAAT 1134
Qy      1149  GCGCGACCTCTACCAACCGTTGTTCAACTTCAAAACAGAGTGTCTGGGCTTCAACCGAG 1208
Db      1135  GGTGCTGTCATTCACCGCATTTGTTCAATTTCAAAACAGAGTTAGGTGGAGCTTCAATGGAG 1194
Qy      1209  CTTATCAACAGGCTTAATACCAAGAGCATGTGAGGCGACAGATGAATGGTGGCTTTCCA 1265
Db      1195  CTATCAACAGGCTTAATACCTGAGCATGTGAGGAGCAAAATGACACAGANTTACAA 1251

RESULT 3
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LOCUS   AV782577              709 bp      mRNA      linear      EST 28-MAR-2002
DEFINITION AV782577 RAFL4 Arabidopsis thaliana cDNA clone RAFL04-19-E04 '3',
            mRNA sequence.
ACCESSION AV782577.1 GI:19801367
VERSION   AV782577
KEYWORDS  EST.
SOURCE    Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 709)
AUTHORS   Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
            Oono,Y., Sakurai,T., Carinici,P., Kawai,J., Itoh,M., Ishii,Y.,
            Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
            and Shinozaki,K.
TITLE     Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL   Unpublished (2002)
COMMENT   Contact: Motoaki Seki
            Plant Functional Genomics Research Group
            RIKEN Genomic Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: 81-298-36-4359
            Fax: 81-298-36-9060
            Email: mseki@rtc.riken.go.jp
            An Arabidopsis full-length cDNA library was constructed essentially
            as reported previously (Seki et al., 1998). This clone is in a
            modified pBluescript vector as a SstI/XhoI insert. Please visit our
            web site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for
            further details.

FEATURES             Location/Qualifiers
     source            1..709
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /db_xref="taxon:3702"
                     /clone="RAFL04-19-E04"
                     /dev_stage="rosette plants"
                     /lab_host="SOLR"
                     /clone_lib="RAFL4"
                     /notes="Site 1: SstI; Site 2: XhoI; subjected to
                     cold-treated (1,2,5,10,24 hr)"

ORIGIN

Query Match      43.1%; Score 704.8; DB 1; Length 709;
Best Local Similarity 99.7%; Pred. No. 9.9e-132;
Matches 706; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      849  GGCAGCCGTTATTCGCGGAGAAAATTCGTGGACCGACGCTAGTGGAGATCATAAAGTT 908
Db      709  GGCAGCCGTTATTCGCGGAGAAAATTCGTGGACCGACGCTAGTGGAGATCATAAAGTT 650

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Qy	909	CTTGTTGTA	CTCAA	CTCGGGA	AGAAAT	CGGTG	CATGA	ACCA	CAACT	CA	CAGACT	TCAGA	968
Db	649	CTTGTTGTA	CTCAA	CTCGGGA	AGAAAT	CGGTG	CATGA	ACCA	CAACT	CA	CAGACT	TCAGA	590
Qy	969	TTCCCA	CAAAAT	CAAAG	CCCA	CCCTT	GGCATA	AGGTTTT	TCCAC	AGCGGAT	GCCTCC	GGAA	1028
Db	589	TTCCCA	CAAAAT	CAAAG	CCCA	CCCTT	GGCATA	AGGTTTT	TCCAC	AGCGGAT	GCCTCC	GGAA	530
Qy	1029	GCAATT	GCACTT	GCATCT	CGGCTT	CTTT	CAAT	PACT	CACAA	GTCTAC	GTGTG	CAC	1088
Db	529	GCAATT	GCACTT	GCATCT	CGGCTT	CTTT	CAAT	PACT	CACAA	GTCTAC	GTGTG	CAC	470
Qy	1089	GAGCAT	GTGG	CGCA	TCCG	TTTT	TTT	CAAT	GAAT	CCGTG	AGCAAA	TGCTG	1148
Db	469	GAGCAT	GTGG	CGCA	TCCG	TTTT	TTT	CAAT	GAAT	CCGTG	AGCAAA	TGCTG	410
Qy	1149	GGCCG	ACTCT	TAC	CAC	CGT	TGTT	CAAC	CTT	CNA	ACAG	GTGTCT	1208
Db	409	GGCCG	ACTCT	TAC	CAC	CGT	TGTT	CAAC	CTT	CNA	ACAG	GTGTCT	1208
Qy	1209	CTTAT	CAAC	AGGCT	TAAT	TAC	CAG	AGCAT	GTG	AGG	CGC	ACAGAT	1268
Db	349	CTTAT	CAAC	AGGCT	TAAT	TAC	CAG	AGCAT	GTG	AGG	CGC	ACAGAT	290
Qy	1269	CAAGCT	GGAC	CCCT	TAGA	AAAG	CGAT	CT	CGAG	ATG	CTTT	TCCAG	1328
Db	289	CAAGCT	GGAC	CCCT	TAGA	AAAG	CGAT	CT	CGAG	ATG	CTTT	TCCAG	230
Qy	1329	GGAA	TGA	AGG	AGG	AGAT	TACT	CTCT	CTG	ATTA	CTTA	AGTAT	1388
Db	229	GGAA	TGA	AGG	AGG	AGAT	TACT	CTCT	CTG	ATTA	CTTA	AGTAT	170
Qy	1389	AGAT	GAT	GTCT	CTCC	TTAG	ACGT	GG	CCAA	TTCAG	CTTTT	TG	1448
Db	169	AGAT	GAT	GTCT	CTCC	TTAG	ACGT	GG	CCAA	TTCAG	CTTTT	TG	110
Qy	1449	ATTG	TG	TCCCA	TATTA	TATCT	TTTT	TG	TTC	CAC	TACT	TG	1508
Db	109	ATTG	TG	TCCCA	TATTA	TATCT	TTTT	TG	TTC	CAC	TACT	TG	50
Qy	1509	TCAG	TAT	TG	TAT	ATG	TTTT	TG	TCT	TGA	ATTA	GAA	1556
Db	49	TCAG	TAT	TG	TAT	ATG	TTTT	TG	TCT	TGA	ATTA	GAA	2
RESULT 4	CL957492	CL957492	LOCUS	DEFINITION	CL957492	CL957492	CL957492.1	GI:52369867	GSS.	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	
LOCUS	CL957492	CL957492	LOCUS	DEFINITION	CL957492	CL957492	CL957492.1	GI:52369867	GSS.	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	
DEFINITION	CL957492	CL957492	DEFINITION	CL957492	CL957492	CL957492	CL957492.1	GI:52369867	GSS.	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	
ACCESSION	CL957492	CL957492	ACCESSION	CL957492	CL957492	CL957492	CL957492.1	GI:52369867	GSS.	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	
VERSION	CL957492	CL957492	VERSION	CL957492	CL957492	CL957492	CL957492.1	GI:52369867	GSS.	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	
KEYWORDS	CL957492	CL957492	KEYWORDS	CL957492	CL957492	CL957492	CL957492.1	GI:52369867	GSS.	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	
SOURCE	CL957492	CL957492	SOURCE	CL957492	CL957492	CL957492	CL957492.1	GI:52369867	GSS.	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	
ORGANISM	CL957492	CL957492	ORGANISM	CL957492	CL957492	CL957492	CL957492.1	GI:52369867	GSS.	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	
REFERENCE	CL957492	CL957492	REFERENCE	CL957492	CL957492	CL957492	CL957492.1	GI:52369867	GSS.	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	
AUTHORS	CL957492	CL957492	AUTHORS	CL957492	CL957492	CL957492	CL957492.1	GI:52369867	GSS.	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	Oryza sativa (indica cultivar-group)	
TITLE	CL957492	CL957492	TITLE	CL957492	CL957492	CL957492	CL957492.1	GI:52369867	GSS.	Oryza sativa (ind			


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BP560588      684 bp      mRNA      linear      EST 20-JUN-2004
LOCUS          BP560588 RAFL4 Arabidopsis thaliana cDNA clone RAFL04-12-J20 5',
DEFINITION     mRNA sequence.
ACCESSION      BP560588
VERSION        BP560588.1 GI:48976354
KEYWORDS       EST.
SOURCE         Arabidopsis thaliana (thale cress)
ORGANISM       Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE      1 (bases 1 to 684)
AUTHORS        Seki,M., Narusaka,M., Kamiya,A., Ishida,J., Satou,M., Sakurai,T.,
                Nakajima,M., Enju,A., Kiyama,K., Oono,Y., Muramatsu,M.,
                Hayashizaki,Y., Kawai,J., Carninci,P., Itoh,M., Ishii,Y.,
                Arakawa,T., Shibata,K., Shinagawa,A. and Shinozaki,K.
TITLE          Functional annotation of a full-length Arabidopsis cDNA collection
JOURNAL        Science 296 (5565), 141-145 (2002)
MEDLINE        21932900
PUBMED         11910074
COMMENT        Contact: Motoaki Seki
                Plant Functional Genomics Research Group
                RIKEN Genomic Sciences Center
                3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                Tel: 81-298-36-4359
                Fax: 81-298-36-9060
                Email: msek@rtc.riken.go.jp
                Please visit our web site (http://pfgweb.gsc.riken.go.jp/) for
                further details.
FEATURES       Location/Qualifiers
                1..684
                /organism="Arabidopsis thaliana"
                /mol_type="mRNA"
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                /lab_host="SOLR"
                /clone_lib="RAFL4"
                /notes="Site 1: SctI; Site 2: XhoI; subjected to
                cold-treated (1,2,5,10,24 hr)"
ORIGIN
Query Match      41.6%; Score 680.4; DB 5; Length 684;
Best Local Similarity 99.6%; Pred. No. 8.1e-127;
Matches 681; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 774 ATCTTTGGTCCACAGAGTATACATCCATTGATATATGGTCTGCTGTTGTGTTCTG 833
DB 1 ATCTTTGGTCCACAGAGTATACATCCATTGATATATGGTCTGCTGTTGTGTTCTG 60
QY 834 GCAGAGTACTCTTGGGAGCGTTATTCGCGGAGAAATTTCTGTGACGAGCTAGTG 893
DB 61 GCAGAGTACTCTTGGGAGCGTTATTCGCGGAGAAATTTCTGTGACGAGCTAGTG 120
QY 894 GAGATCATAAAGTCTTGTGACTCCAACTCGCGAAGAAATCCGTCGATGAACCCAAAC 953
DB 121 GAGATCATAAAGTCTTGTGACTCCAACTCGCGAAGAAATCCGTCGATGAACCCAAAC 180
QY 954 TACACAGACTTTCAGATTCACCAAAATCAAGCCACCCCTTGGCATGAAGGTTTTCCACAAG 1013
DB 181 TACACAGACTTTCAGATTCACCAAAATCAAGCCACCCCTTGGCATGAAGGTTTTCCACAAG 240
QY 1014 CGGATGCTCCGAGAGCATTGACCTTGCATCTCGGCTTCTTCAATCACTACCAAGTCTA 1073
DB 241 CGGATGCTCCGAGAGCATTGACCTTGCATCTCGGCTTCTTCAATCACTACCAAGTCTA 300
QY 1074 CGTTGCATCGCTCCGAGGAGTGGCGCATGTCGGTTTTTCAATGAATCCGTGAGCCAAAT 1133
DB 301 CGTTGCATCGCTCCGAGGAGTGGCGCATGTCGGTTTTTCAATGAATCCGTGAGCCAAAT 360
QY 1134 GCTCGTCTTCCAAATGCGGACCTCTACCAACCGTTGTTCAACTTCAACAAAGAGTTGTCT 1193

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DB 361 GCTGCTGTCTCCAAATGGCGGACCTCTACACACGGTTGTTTCAACTTCAAAACAGAGTTGTCT 420
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DB 421 GGGGCTTCCACGGAGCTTATCAACAGGCTAAATACAGAGCATGTGAGGCGCAGAGTGAAT 480
QY 1254 GGTGGCTTTCCATTTCAAGCTGGACCCCTAGAAAAGCGATCTCGAGATGCTTTTCCAGAGC 1313
DB 481 GGTGGCTTTCCATTTCAAGCTGGACCCCTAGAAAAGCGATCTCGAGATGCTTTTCCAGAGC 540
QY 1314 AAAATGCCGCCCTTATGGAATGAAGAGAGGAGATTTACTTCTCTGATTAACCTAAGTA 1373
DB 541 AAAATGCCGCCCTTATGGAATGAAGAGAGGAGATTTACTTCTCTGATTAACCTAAGTA 600
QY 1374 TCAGCTTCTGAGAAGAGATGATGTCCTCCCTTAGACGTGGCCAAATTCAGCTTTTGTAGA 1433
DB 601 TCAGCTTCTGAGAAGAGATGATGTCCTCCCTTAGACGTGGCCAAATTCAGCTTTTGTAGA 660
QY 1434 AATCAGGAGGCGATGATTTGTGTCC 1457
DB 661 AATCANGANGCGATGTTGGGTCC 684

RESULT 7
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LOCUS          AV782869 RAFL5 Arabidopsis thaliana cDNA clone RAFL05-02-L16 3',
DEFINITION     mRNA sequence.
ACCESSION      AV782869
VERSION        AV782869.1 GI:19801659
KEYWORDS       EST.
SOURCE         Arabidopsis thaliana (thale cress)
ORGANISM       Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE      1 (bases 1 to 690)
AUTHORS        Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,
                Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
                Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
                and Shinozaki,K.
TITLE          Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL        Unpublished (2002)
COMMENT        Contact: Motoaki Seki
                Plant Functional Genomics Research Group
                RIKEN Genomic Sciences Center
                3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
                Tel: 81-298-36-4359
                Fax: 81-298-36-9060
                Email: msek@rtc.riken.go.jp
                An Arabidopsis full-length cDNA library was constructed essentially
                as reported previously (Seki et al., 1998). This clone is in a
                modified plasmid vector as a SctI/XhoI insert. Please visit our
                web site (http://www.gsc.riken.go.jp/e/plant/index\_e.html) for
                further details.
FEATURES       Location/Qualifiers
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                /notes="Site 1: SctI; Site 2: XhoI; subjected to
                dehydration-treated (1,2,5,10,24 hr)"
ORIGIN
Query Match      41.1%; Score 673.2; DB 1; Length 690;
Best Local Similarity 99.4%; Pred. No. 2.3e-125;
Matches 686; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
QY 868 GAGAAAATTTCTGTGGACGAGTAGTGGAGATCATAAAGGTTTCTTGTTACTCAACTCGCG 927

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Db 690 GAGAAATTTCTGTGACCAAGCTAGTGGAGATCATAAAGTTCTTGTGATCTCCAATCGCG 631
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Db 630 AAGAAATCGGGTGATGAACCAACTACAGACTTCAGATTCACCAAAATCAAAGCC 571
QY 987 CACCTTGGCATAGTTTCCACAGCGGATGCTCCGAGACCATTCACCTTGCATCT 1046
Db 570 CACCTTGGCATAGTTTCCACAGCGGATGCTCCGAGACCATTCACCTTGCATCT 511
QY 1047 CGGCTTCTTCAATCTACCAAGTCTACGTTGCACTCGCTCGAGCATGTCGATCG 1106
Db 510 CGGCTTCTTCAATCTACCAAGTCTACGTTGCACTCGCTCGAGCATGTCGATCG 451
QY 1107 TTTTCAATGAATCGTGGAGCAAAATGCTGCTTCCAAATGGCGACCTCTACACCG 1166
Db 450 TTTTCAATGAATCGTGGAGCAAAATGCTGCTTCCAAATGGCGACCTCTACACCG 391
QY 1167 TTGTTCAACTTCAACAGAGTTGCTGGGCTTACCGAGCTTATCAAGGCTAATA 1226
Db 390 TTGTTCAACTTCAACAGAGTTGCTGGGCTTACCGAGCTTATCAACAGGCTAATA 331
QY 1227 CCAGAGCATGTCAGGCGACAGATGAATGCTGCTTCCATTTCAAGCTGGACCTAGAAA 1286
Db 330 CCAGAGCATGTCAGGCGACAGATGAATGCTGCTTCCATTTCAAGCTGGACCTAGAAA 271
QY 1287 AGCGATCTCGAGATGCTTTTCCAGAGCAAAATGCGGCTTATGGAATGAAGGAGGGAG 1346
Db 270 AGCGATCTCGAGATGCTTTTCCAGAGCAAAATGCGGCTTATGGAATGAAGGAGGGAG 211
QY 1347 ATTACTTCTCTGATTAATCAAGTATCAAGTCTTGAAGAGATGATGCTCTCTCT 1406
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Db 90 CTTTTTGTCTACTGACTTGTAGAGAGATCTTTTCTCTGTATCATGATTTGTATATGT 31
QY 1527 TTTGCTCTTGAATGAACAAATCGATTC 1556
Db 30 TTTGCTCTTGAATGAACAAATCGATTC 1

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RESULT 8
BP560678 683 bp mRNA linear EST 20-JUN-2004
LOCUS BP560678 RAFL4 Arabidopsis thaliana cDNA clone RAFL04-19-E04 5',
DEFINITION mRNA sequence.
ACCESSION BP560678
KEYWORDS BP560678.1 GI:48976444
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 683)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
21932900
MEDLINE 11910074
PUBMED
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center

```

3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: mseki@rtc.riken.go.jp
 Please visit our web site (<http://pfgweb.gsc.riken.go.jp/>) for further details.

FEATURES

source
 1..683
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="RAFL04-19-E04"
 /dev_stage="rosette plants"
 /lab_host="SOLR"
 /clone_lib="RAFL4"
 /note="Site 1: SstI; Site 2: XhoI; subjected to cold-treated(1,2,5,10,24 hr)"

ORIGIN

Query Match 40.4%; Score 660.2; DB 5; Length 683;
 Best Local Similarity 99.4%; Pred. No. 9.7e-123;
 Matches 662; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 1 TTTACTCTTTTCAGTCAGAGAGAGAGTTAGAGCTGTAAGGCACATGACTTCGATACCAT 60
Db 17 TTTACTCTTTTCAGTCAGAGAGAGAGTTAGAGCTGTAAGGCACATGACTTCGATACCAT 76
QY 61 TGGGCGCTCTTCAGCTCCGCTCTTTAGTCTCTTCAGCCGCGCATCTTCAGCGCGAGATT 120
Db 77 TGGGCGCTCTTCAGCTCCGCTCTTTAGTCTCTTCAGCCGCGCATCTTCAGCGCGAGATT 136
QY 121 CTTTGAAGAGCTGCTCCGATATAGACAACAGCAAGGAATGTCGCTGCTGTATAGAG 180
Db 137 CTTTGAAGAGCTGCTCCGATATAGACAACAGCAAGGAATGTCGCTGCTGTATAGAG 196
QY 181 GAATGATGCTGTTACCGGTGACATAATTTCTACTACAAATGGAGGCAAAATGCTGAAC 240
Db 197 GAATGATGCTGTTACCGGTGACATAATTTCTACTACAAATGGAGGCAAAATGCTGAAC 256
QY 241 CTAAACAGACCATTAGTTTACATGCGCGAACGTTGTTGGAAACAGGATCATTTCGGAATTG 300
Db 257 CTAAACAGACCATTAGTTTACATGCGCGAACGTTGTTGGAAACAGGATCATTTCGGAATTG 316
QY 301 TATTCCAGGCAAAATGCTTGAAGAACTGGAGAACTAGTAGCCCAATTAAGAGGTTTTCGAAG 360
Db 317 TATTCCAGGCAAAATGCTTGAAGAACTGGAGAACTAGTAGCCCAATTAAGAGGTTTTCGAAG 376
QY 361 ATCGCGTTTATAAAACCGAGAGTTGCAATTAATCGGACTTAATGCAACCATCCAAATGTCG 420
Db 377 ATCGCGTTTATAAAACCGAGAGTTGCAATTAATCGGACTTAATGCAACCATCCAAATGTCG 436
QY 421 TTTCTTGAAGCATTTGTTCTTCTACAAAGCTAGAGATGAGCTCTTCTCTCAATCTCG 480
Db 437 TTTCTTGAAGCATTTGTTCTTCTACAAAGCTAGAGATGAGCTCTTCTCTCAATCTCG 496
QY 481 TTATGGAGTATGTACAGAGACATTTGTACCGGGTTTGAAGCACTATATAGTCTCAAAACC 540
Db 497 TTATGGAGTATGTACAGAGACATTTGTACCGGGTTTGAAGCACTATATAGTCTCAAAACC 556
QY 541 AGCGATGCTCTATCTTCTATGTCAAACTTTACACATCAAAATCTTTCAGAGCTTTGGCTT 600
Db 557 AGCGATGCTCTATCTTCTATGTCAAACTTTACACATCAAAATCTTTCAGAGCTTTGGCTT 616
QY 601 ATATCTACTGCTCTCTGCTGCTGTCGCCACAGAGATATAAAACCAACCAAAATCTTTTGGTTG 660
Db 617 ATATCTACTGCTCTCTGCTGCTGTCGCCACAGAGATATAAAACCAACCAAAATCTTTTGGTTG 676
QY 661 ATCCCC 666
Db 677 ATCCCC 682

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RESULT 9

AY104068	AV104068	Zea mays	1666 bp	mRNA	linear	HTC 16-OCT-2002					
LOCUS	PCO083097	mRNA sequence.									
DEFINITION	AY104068	Zea mays									
ACCESSION	AY104068.1	GI:21207146									
VERSION	HTC.										
KEYWORDS	HTC.										
SOURCE	Zea mays										
ORGANISM	Zea mays										
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.										
AUTHORS	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.										
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes										
JOURNAL	Unpublished (2002)										
REFERENCE	2 (bases 1 to 1666)										
AUTHORS	Coe, E.H.										
TITLE	Direct Submission										
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA										
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at WSL, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.										
FEATURES	Location/Qualifiers										
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	/db_xref="MaizeDB:634655"										
	/db_xref="taxon:4577"										
	/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"										
	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"										
ORIGIN											
Query Match	40.0%; Score 654.6; DB 3; Length 1666;										
Best Local Similarity	75.2%; Pred. No. 1.4e-121;										
Matches	816; Conservative 0; Mismatches 269; Indels 0; Gaps 0;										
QY	177	GAAGGAAATGATGCTGTTACCGGTACATAATTTCTACTACAATTCGAGGCAAAATGGT	236								
Db	260	GAAGGGGAGACCGCTGTGACGGGTACATCATCTCCACCACCATCGCGGGAAGACGGC	319								
QY	237	GAACCTAAACAGACCAATAGTACATGCGCGAAGCGTGTGTTGGAAACAGGATCATTCGGA	296								
Db	320	GAGCCCAAGCGGACCATCAGTTACATGGCAGAAGCGTGTGGGTACGGGCTCATTTGGG	379								
QY	297	ATTGTTATCCAGGCAAAATGCTTTGGAAACCTGGAGAAATCAGTAGGCCATTAAGAAGTTTGG	356								
Db	380	ATCGTCTTCCAGGCTAAGTGTGTTGGAGCTGGAGAGACCTTCGCCCATTAAGAAGTGTCTG	439								
QY	357	CAAGATCGCGTTATAAAACCGAGAGTTTCGAATTAATGGCACTAATGGACCATCCAAAT	416								
Db	440	CAGGATCGCGGTTTACAGAAACCGGAGCTGCACTTATGCGTGCATGGAGCACCCCAAC	499								
QY	417	GTGGTTTCTTGAAGCAATGTTTCTTCTCTACAACTAGAGATGAGCTCTTCTCTCAAT	476								
Db	500	GTCACTGCTTGAAGCACTGCTTCTTCTCAACACGAGCAGGACGAGTTGTTCTTAAAC	559								
QY	477	CTCGTTATGAGTATGTACCAGAGACATTTGTACCGGTTTGAAGCACTACTACTAGTTCA	536								
Db	560	CTTGTCATGGAATTTGTCCCAGACCTGTACCGTGTCTTGAAGCACTACAGCAAGCGC	619								

QY	537	AAACGAGCGATGCTTATCTTCTATGTCAAACTTTACACATACCAAAATCTTTCAGAGCGTTG	596	
Db	620	AAACGAGGATGCTCTTATCTACGCTCAAGCTCTACATGTATCAGCTTTTCAGAGGCCCTA	679	
QY	597	GCTTATATCCATPACTGCTCCTGGTGTCTGCCACAGAGATATAAAACCAAAAATCTTTTG	656	
Db	680	GCTTATATTCATAATATGTTACAGGAGTCTGCCATAGGGATGTAAGGCCACAAAACGTTTTC	739	
QY	657	GTTGATCCCCACACCCATCAGTGAAGCTCTGTGATTTTGGAGTGCAAAAGTACTTGGTG	716	
Db	740	GTTGATCTCTCACCACACAGGTCAGGCTCTGTGACTTTGGTAGCCCAAAAGTCTTGATT	799	
QY	717	AAAGGTGAACCAAAATATATATCTGCTCTCGGTATTTACCGAGCTCCAGAACTCATC	776	
Db	800	CCTGCTGAACCGAACATATCTTTACATATGCTCTCGTATTATTCGTGCTCCAGAGCTCAT	859	
QY	777	TTTGTGTCACAGAGATATACATCATTCATGATATATGCTGTGCTGGTTGTGTTCTGGCA	836	
Db	860	TTTGGAGCGACGAGGATATCAAACTTCAATAGACATATGGTTCAGCTGGCTGTGTTCTAGCT	919	
QY	837	GAGCTACTTCTTTGGGCGAGCGGTTATTTCCCGGGAGAAAATTCCTGTGACCAAGCTAGTGGAG	896	
Db	920	GAGTTGCTTCTTTGGTCAGCCACTGTTTCCGGGAGAGAGTGCTGTTCATCAGTTGGTAGAG	979	
QY	897	ATCATAAAGGTTCTTTGGTACTCCAACTCCGGAAGAAATCCGGTGCATGAACCCAAACTAC	956	
Db	980	ATTATCAAGTTCTTTGGTACTCCAAACCGCTGAGGAGATACGATGATGAATCCCAACTAT	1039	
QY	957	ACAGACTTCAGATTTCCCAAAATCAAAAGCCACCTTGGCATTAAGTTTTCACAAGCGG	1016	
Db	1040	ACTGAGTTTCAGGTTTCTCCAGATAAAGGCTCATCTCGTGGCACAAGATTTTCCACAAGAGA	1099	
QY	1017	ATGCTCTCCGGAAGCCATTGACCTTGCACTTCGCTTCTTCAATATCTCACCAGTCTACGT	1076	
Db	1100	ATGCTCTCTGAAGCCATTGACCTTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCGC	1159	
QY	1077	TGCACTGCGCTCGAGCATGTGGCATCCGTTTTCATTAATGAATCCGTGAGCCAAATGCT	1136	
Db	1160	TGCTCTGCTCTTGAAGCATGCGCTCATCTCCCTTCTTCGATGAGTCGGGACACCGAAGCA	1219	
QY	1137	CGTCTTCCAAATGGCGGACCTCTACCACCGTTGTTTCAACTTCAACAAAGAGTTGTCTGGG	1196	
Db	1220	CGCTTACCAAAAGCGCGCGCTTCCCTCGCTCTTTAACTTCAAGCAAGACTAGCAAT	1279	
QY	1197	GCTTACCGGAGCTTATCAACAGGCTAATACAGAGCATGTGAGGCGACAGATGAATGGT	1256	
Db	1280	GCTCTCCGAGCCTCTGTCAGCAGGCTTGTGCCGAGACATTTAGACGGCAGATCGGTGTC	1339	
QY	1257	GGCTT 1261		
Db	1340	AACCTT 1344		
RESULT 10				
LOCUS	AV822185	658 bp	mRNA	linear EST 01-APR-2002
DEFINITION	AV822185	RAFL5 Arabidopsis thaliana cDNA clone RAFL05-02-L16 5', mRNA sequence.		
ACCESSION	AV822185			
VERSION	AV822185.1	GI:19864218		
KEYWORDS	EST.			
SOURCE	Arabidopsis thaliana (thale cress)			
ORGANISM	Arabidopsis thaliana			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.			
AUTHORS	Seki, M., Naruseaka, M., Iehida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.			
TITLE	Large scale analysis of Arabidopsis full-length cDNA (2002b)			
JOURNAL	Unpublished (2002)			

COMMENT

Contact: Motoaki Seki
Plant Functional Genomics Research Group
Riken Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msekis@tc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a modified plasmid vector as a SstI/XhoI insert. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES

source
Location/Qualifiers
1..658
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAPL05-02-L16"
/dev_stage="rosette plants"
/lab_host="SOLR"
/clone_lib="RAPL5"
/note="Site 1: SstI; Site 2: XhoI; subjected to dehydration-treated(1,2,5,10,24 hr)"

ORIGIN

Query Match 37.9%; Score 620; DB 1; Length 658;
Best Local Similarity 99.7%; Pred. No. 1.2e-114;
Matches 620; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TTTACTCTTTCAGTGAGAGAGAGTGTAGAGCTGTAAAGCACATGACTTCGTATACCAT 60
DB TTTACTCTTTCAGTGAGAGAGAGTGTAGAGCTGTAAAGCACATGACTTCGTATACCAT 96
QY 61 TGGGGCTCTCAGGCTCGCTTTAGTCTCTCAGCGCGCATCTTCACGCGGAGATT 120
DB TGGGGCTCTCAGGCTCGCTTTAGTCTCTCAGCGCGCATCTTCACGCGGAGATT 156
QY 121 CTTTGAAGCTGCTCCGATATAGACACGACGAGAAATGTCTGCTGTATAGAG 180
DB CTTTGAAGCTGCTCCGATATAGACACGACGAGAAATGTCTGCTGTATAGAG 216
QY 181 GAAATGCTGTTACCGGTCTCAATATTTCTACTCAATTTGGAGGCAAAATGTGAC 240
DB GAAATGCTGTTACCGGTCTCAATATTTCTACTCAATTTGGAGGCAAAATGTGAC 276
QY 241 CTAACACAGACATTAAGTACATGCGGCGCAACGTTGTTGGACAGATCATTCGGAATTG 300
DB CTAACACAGACATTAAGTACATGCGGCGCAACGTTGTTGGACAGATCATTCGGAATTG 336
QY 301 TATTCAGGCAAAATGCTTGGAACTGGAGAAATCAGTAGCCATTAAGAGGTTTTGCAAG 360
DB TATTCAGGCAAAATGCTTGGAACTGGAGAAATCAGTAGCCATTAAGAGGTTTTGCAAG 396
QY 361 ATCGCGGTATATAAACCGAGATGTCATTAATCGCATATGACCATCAAAATGG 420
DB ATCGCGGTATATAAACCGAGATGTCATTAATCGCATATGACCATCAAAATGG 456
QY 421 TTTCTTGAAGCATTTGTTCTCTCTACAACTAGAGATGAGTCTTCTCTCAATCTCG 480
DB TTTCTTGAAGCATTTGTTCTCTCTACAACTAGAGATGAGTCTTCTCTCAATCTCG 516
QY 481 TTATGAGATGATACAGAGACATTTGACCGGGTTTTGAAGCACTATATAGTCAAAACC 540
DB TTATGAGATGATACAGAGACATTTGACCGGGTTTTGAAGCACTATATAGTCAAAACC 576
QY 541 ACCGATGCTATCTTATGTCAAACTTTACACATACCAAACTTCAGAGCTTGGCTT 600
DB ACCGATGCTATCTTATGTCAAACTTTACACATACCAAACTTCAGAGCTTGGCTT 636
QY 601 ATATCCATCTGCTCTCTGTGT 622
DB ATATTCATCTGCTCTCTGTGT 658

RESULT 11

CK266410 924 bp mRNA linear EST 03-AUG-2004
LOCUS EST712488 potato abiotic stress cDNA library Solanum tuberosum cDNA
DEFINITION clone POAC457 5' end, mRNA sequence.
ACCESSION CK266410 GI:39823388
VERSION CK266410
KEYWORDS Solanum tuberosum (potato)
SOURCE Solanum tuberosum
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B. Generation of ESTs from abiotic stressed potato tissue Unpublished (2003)
CONTACT: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics Institute via <http://genome.arizona.edu/orders/>.
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source
Location/Qualifiers
1..924
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAC457"
/tissue type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="potato abiotic stress cDNA library"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI; supplier: Solanum tuberosum var. Kennebec plants were grown from cuttings on a 16hr light/8 hr dark cycle at 25 C for 3-4 weeks. Abiotic stress conditions were applied to four separate sets of plants. Set 1 involved saturation of the soil with 150 mM NaCl and tissues were harvested at following application of the salt stress (leaves: 2hr, 6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d). Set 2 were grown under the standard conditions and then were water stressed by withdrawal of further watering application. Drought stressed plants were harvested after cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d and 5d). Set 3 were grown under the standard conditions and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

ORIGIN

Query Match 37.6%; Score 615; DB 7; Length 924;
Best Local Similarity 79.3%; Pred. No. 1.3e-113;
Matches 729; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 286 GATCATTCGGATTTGTATCCAGCCAAATCTTGGAACTGGAGAGTGTGGCCATTA 345
DB TTTCTTGGATAGTGTTCAGGCAAAATCTTGGAACTGGAGAGTGTGGCCATTA 60
QY 346 AGAAGTTTTCAGAGTCGCGTTTATAAAACCGAGAGTTGCAATTAATGCCACTAAATGG 405
DB AGAAGTTTTCAGAGTCGCGTTTATAAAACCGAGAGTGTGCAATTAATGCCACTAAATGG 120
QY 406 ACCATCCAAATGTGGTTCCTTGAAGCATTTGTTCTTCTTCTACACGACTAGAGATGAGC 465

Db 121 ATCAACCAATGTCATTACTCTAAAGCACTGCTCTTTCCACGACTAGTAGAGATGAGC 180
QY 466 TCTTCTCTCAATCTCGTTATGGAGTAGTACCAGAGACATGTACCGGTTTGAAGCACT 525
Db 181 TTTTCTCTAATTTGGTCATGGATTATGTCCTGAAAGTTTATACAAAGTTTAAAGCACT 240
QY 526 ATACTAGTTCAACACGAGATGCGCTATCTTCTATGTCAAACTTTACACATACCAATCT 585
Db 241 ATAGCAATCAATCAAGATGCCACTCATATATGTCAAACTTTACATGTATCAGATAT 300
QY 586 TCAGAGGCTTGGCTTATATCCATPACTGCTCTGCTGCTGCTGCCACAGAGATATAAAACAC 645
Db 301 TCAGAGGCTGCTTACATTAATGTTCCAAAGATTTGCCATAGAGATGTGAACCTC 360
QY 646 AATCTTTTGGTTGATGCCACACCCATCAGTGTAGCTCTGTGATTTTGGAGTGCAA 705
Db 361 AATCTTTTGGTTGATGCCCTCTGACCCATCAAGTCAAGTATGTGATTTTGGAGTGCAA 420
QY 706 AAGTACTGTTGAAGTGAACCAACATATCATATATCTGCTCTCGTATATCCGAGCTC 765
Db 421 AAGTCTGTTGAAGTGAAGCAAAATTTTCGTACATTTGCTCTCGTACTACAGAGCTC 480
QY 766 CAGAATCTATCTTTGTTGGCCACAGAGTATACATCATCAATGATATATGTTCTGCTGGTT 825
Db 481 CAGAATCTATTTGTTGGCCACAGATATACATCAATGATATTTGTTGACAGGCT 540
QY 826 GTGTTCTGGCAGAGTACTTCTTGGGAGCGGTTATTCGGGAGAGAAATTCGTGGACC 885
Db 541 GTGTCCTTGTGAGCTTCTTCTGGGAGCGGCTCTTTCCTGGCGAAATTCGGTAGACC 600
QY 886 AGCTAGTGGAGATCATAAAGTCTTGGTACTCCAACTCGAGAGAAATCCGGTGCATGA 945
Db 601 AACTGTTGGAGATCATCAAGTCTTGGTACTCTTCTGCGGAAGAAATTCGATGATGA 660
QY 946 ACCCAAACTACACAGACTTCAGATTTCCCAAAATCAAGCCCACTTGGCATTAAGGTTT 1005
Db 661 ACCCAAACTACACAGATTTTCAGATTTCCCAAGATTAAGCTCATCTTGGCACAAGTAT 720
QY 1006 TCACAAGCGGATGCTTCGGAGAGCCATTTGACCTTGATCTCGGCTTCTCAATCTCAC 1065
Db 721 TCCATAAAGAAATGCTCTCTGAAAGCAATTTGATCTGCTCAGCGCTTCTTCAATTTTAC 780
QY 1066 CAGTCTACCTGCTGCTGCTGCGGAGCATGCGCATCCGTTTTCATGAACTCCGCTG 1125
Db 781 CAGTCTTCTGCTGCTGCTGCGGAGCATGCGCATCAATTCATTTGATGAGCTTCGCTG 840
QY 1126 AGCCAAATGCTGCTTCTCCAAATGGCGAGCTCTTACCAACGTTTGTTCAACTTCAAAACAG 1185
Db 841 AGCCAAATGCTGCTTCTCCCTTATGAGAGTCCATTTCCACCTCTTTTCACTTTAAACAG 900
QY 1186 AGTTGCTGCGGCTTCACC 1204
Db 901 AGTTAACTGGAGCTTACC 919

RESULT 12

CNS09YSF 1638 bp mRNA linear HTC 06-FEB-2004
LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
DEFINITION GSLTSL912E05 of Adult vegetative tissue of strain col-0 of
Arabidopsis thaliana (thale cress).
BX831446
VERSION BX831446.1 GI:42455013
LOCUS HTC; GSLT cDNA.
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
1 (bases 1 to 1638)
REFERENCE Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C.,
Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V.,

TITLE Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
JOURNAL Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences:
REFERENCE A Combined Approach to Evaluate and Improve Arabidopsis Genome
AUTHORS Annotation
JOURNAL Unpublished
TITLE Genoscope.
COMMENT Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out
full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli
V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,
Schachter V., Weissenbach J., Salanoubat M.
URUG INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis
genome released by MIPS (Munich Information center for Protein
Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_FF/Full
length
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

FEATURES

source

1..1638
/organism="Arabidopsis thaliana"
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/strain="Col-0"
/db_xref="taxon:3702"
/clone="GSLTSL912E05"
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complement(1..1638)
/gene="At5G26751"

gene

ORIGIN

Query Match 36.8%; Score 602.2; DB 3; Length 1638;
Best Local Similarity 72.3%; Pred. No. 5.1e-111;
Matches 797; Conservative 0; Mismatches 303; Indels 3; Gaps 1;
QY 148 ACACAAGGAAATGCTGCTGCTGTTATAGAAGGAAATGATGCTTACCGGTACATAA 207
Db 322 ACGATAAAGAAATGGAAGCGACAGTGTAGATGGAATGAAACAGAGACTGGACATATCA 381
QY 208 TTTTCTACTAATTGAGGCAAAATGTTGAACCTTAAACAGACCATAGTTACATGGCCG 267
Db 382 TTGTGACTACTATTTGGTGTAGAAATGGCCAAACCAAAACAGACAATTAGCTACATGCTG 441
QY 268 AACGCTGTTGTGGAACAGGATCAATTCGGAATTTGATTTCCAGGCAAAATGCTTGGAAACTG 327
Db 442 AGCGTGTGTTGTGTACCGATCTTTTGGTGTGTTGTTCCAGGAAATGCTTTGAGACAG 501
QY 328 GAGAATCAGTAGCCATTAAAGAGGTTTTCGAAGATCCCGTTATATAAAACCGAGAGTTGC 387
Db 502 GAGAAACTGTTGCGATAAAGAAAGTTTTCACAGATAGGAGGTACAAGAACCGTGAGCTTC 561
QY 388 AATTAATGCACTAATGGAACCATCCAAATGTGTTTCTTGAAGCATTTGTTTCTTCTCTA 447
Db 562 AAACCATGAGGCTACTTGACCATCTTAATGTTGTGCTCTGAAACCAATTTGTTCTTCTCA 621
QY 448 CAACGACTAGAGATGAGCTTCTCTCAATCTCGTTATGGAGTATGTACACAGACATTTGT 507
Db 622 CCACTGAAAGATGAGCTTTTACTCAATCTTGTCTTGTGATGAGTTCAGGAACTGTTTC 681
QY 508 ACCGGGTTTGAAGCACTATACATAGTTCAAAACCGAGATGCGCTATCTTCTATGTCAAC 567
Db 682 ATCGTGTATCAAACTCAACACTCAACAACTGAATCAGAGAAATGCTCTTATATGCGTCAAC 741
QY 568 TTATACATACCAAACTTTCAGAGGCTTGGCTTATATCCATATGCTCTCGTGGTGTCTGCC 627
Db 742 TTATACATATCAGATCCTTAGAGCCTTATCTTACATTCACCGATGCAATGCAATGGTGTGTC 801

QY 628 ACAGAGATATAAAACCAACAAATCTTTTGGTGTATCCACACCCATCAGTGTAAAGCTCT 687
 Db 802 ATCGTGACATATAAACTCAAACTGTTGGTAAATCCGCACACTCATCAAGTAAAGCTAT 861
 QY 688 GTGATTTTGGAAAGTCAAAAGTACTGGTGAAGGTGAACCAACATATATATATCTGCT 747
 Db 862 GTGGTTTGGAAAGTCAAAAGTATTGGTAAAGGAGAACCAAACTTTCTTACATCTGCT 921
 QY 748 CTCGGTATTACCGAGTCCAGAACTCATCTTTGGTGGCCACAGAGTATACATCATCTG 807
 Db 922 CGAGGTATTACAGAGCACCTGAATCATCTTTGGAGCAACCGAGTATACAGAGCCATTG 981
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 Db 982 ATGCTGGTCTGAGAGTGTGTTAGCTGAACTATTGCTTGGACAGCCCTTTGTTCCCTG 1041
 QY 868 GAGAAATTTCTGTGGACCACTAGTGGAGATCATAAAGTCTTGTGTAATCCAACTCGCG 927
 Db 1042 GTGAGAGCGGTGTGATCAACTTGTAGAGATTATCAAGTCTTGGGAACGCTACTAGAG 1101
 QY 928 AGAAATCCGGTGCATGAACCCAACTACAGACTTACAGATTCCCAAAATCAAGGCC 987
 Db 1102 AAGAAATCAAGTGCATGAACCCAACTACAGGAATTCAATTTCCCTCAGATTAAAGCTC 1161
 QY 988 ACCCTGGCATTAAGTTTTCACACAGCGATGCTCCGGAAGCCATTGACCTTGCATCTC 1047
 Db 1162 ATCCATGGCACAGATTTTTCACAAACGCAATGCTCCAGAGCTGTGTTGGTCTCAA 1221
 QY 1048 GCGTCTTCAATACTCACCAGTCTACGTTGCACTGCGCTCCAGGCGATGCGGCACTCGGT 1107
 Db 1222 GACTTCTTCAATCTCTTATCTACGAGTGGCGCTCTCGACATATTAGTCCACCAT 1281
 QY 1108 TTTTCAATGAATCCGTGAGCCAAATGCTGCTTTCCTCAAAATGCCGACCTTACCAACGT 1167
 Db 1282 TCTTTGATGAGTTAAGAGACCCAAACGACGCTACCTTAATGAGCTTTCTTCCACCGC 1341
 QY 1168 TGTTCAACTTCAA--ACAAGAGTTCTGCGGCTTCCCGGCTTACCGGCTTATCACAGCTTA 1224
 Db 1342 TTTTCAACTTCAAGCTTCAAGAGCTGAAAGGTGTACCATTTGAGAGTGTAGTAAAGTTAG 1401
 QY 1225 TACCAGAGCATGTAGCGGACAG 1247
 Db 1402 TACCTGAGCATGCAAGGAGCAG 1424

RESULT 13

AV103545
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AY103545 1967 bp mRNA linear HTC 16-OCT-2002
 Zea mays P0153236 mRNA sequence.
 AY103545
 AY103545.1 GI:21206623
 HTC.
 Zea mays
 Zea mays

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
 If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizenap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat

Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.
 Location/Qualifiers
 1..1967

FEATURES

source

/organism="Zea mays"
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 /db_xref="taxon:4577"
 /clone_lib="Maize Mapping Project/DuPont Cornsensus Library"
 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 36.6%; Score 598.2; DB 3; Length 1967;
 Best Local Similarity 73.6%; Pred. No. 3.3e-110;
 Matches 762; Conservative 0; Mismatches 273; Indels 0; Gaps 0;
 QY 148 ACGACAAGAAATGCTGCTGTATAGAGGAAATGATGCTGTACCGGTCAATAA 207
 Db 457 ATGATAGGAAGTTGAAGCAACCATTAATTATGGGAAGGACTGAACCTGGGCATATA 516
 QY 208 TTTCTACTAATTTGGAGGCAAAATGTTGAACCTTAAACAGACCAATTAGTTACATGGCG 267
 Db 517 TTGTCACCACACTACTGTTGGCAAGATGTTCAACCAAAACAGACAGTACATGGCTG 576
 QY 268 AACGTGTTTGGAAACAGATCATTTCCGAATTTGATTTCCAGGCAAAATGCTTGGAACTG 327
 Db 577 AGCGCATTTGTAAGTCAAGGTTCTTTTGGGATGCTTCCAGGCCAAGTGTTTGGAACGG 636
 QY 328 GAGATCATGTAGCCATTAAAGAGGTTTTCGAAGATCGCGCTTATAAAACCCAGAGTTGC 387
 Db 637 GTGACATGTTGCCATAAAGAGGTTCTTCAAGACAAGGTTCAAGAACCCGACGACG 696
 QY 388 AATTAAATCGCAATAATGACCATCCAAATGTGGTTTCTTGAAGCATTTGTTCTCTTA 447
 Db 697 AGACCATGCGCTTCTTGACCAACCTAATGTTGTTGCTTTGAAGCATTTGCTTTTCAA 756
 QY 448 CAACGACTAGAGATGAGCTTCTCCTCAATCTGTTATGGAGTATGTACCAAGACATTTG 507
 Db 757 CTACTGAGAAGGATGAGCTTTATCTGAACCTTGGTCTTGAAGTATGTTCCGAGACAGTTC 816
 QY 508 ACCGGTTTGAAGCACTATATAGTTCAAAACCCAGCGATGCTATCTTCTATGTCAAA 567
 Db 817 ATCGAGTTGTGAACATCACAAACAGATGCACCAAGCATGCCACTTATTTATGTGAAG 876
 QY 568 TTTACACATACCAAACTTTTCAGAGGCTTTGGCTTATATCCATACATGCTCTCTGTTGCTGCC 627
 Db 877 TTTATATGACAGATATGTAGAGCATTTGGCTTACATTTCAATGTTACTACTCGGTGCTGCC 936
 QY 628 ACAGAGATATAAACCAACAAATCTTTTGGTGTATGCCACCAACCATCAGTGTAAAGCTCT 687
 Db 937 ACAGAGATATAAAGCCACAAATCTTCTGTGTGAACCCACACACACCCAGCTTAAATAT 996
 QY 688 GTGATTTTGAAGTCAAAAGTACTGTTGAAGGTGAACCAACATATATATATCTGCT 747
 Db 997 GTGATTTTGGTAGTCAAAAGTTCTGTTCAAGGGGGAACCAACATATATATATCTGCT 1056
 QY 748 CTCGGTATTACCGAGCTCCAGAACTCATCTTTTGGTGGCCACAGAGTATATCATCATCTG 807
 Db 1057 CGGATATATAGGCTCCAGAGCTCATATTTTGGTGGCCACTGAGTATACCAAGCATTTG 1116
 QY 808 ATATATGCTGCTGTTGTTGTTTGGCAGAGCTACTTCTTGGGAGCGGCTTATTTCCCGG 867
 Db 1117 ACATTTGCTGCTGATGTTGTTCTTGTGAGCTTATGCTAGGCGAGCGCTTTGTTTCCGG 1176
 QY 868 GAGAAATTTCTGTCAGCAGCTAGTGGAGATCATAAAGTCTTCTGTTACTCTCAACTCGG 927
 Db 1177 GTGAAAGTGGTGGACCAACTTTGTTGAATCATCAAGGTTCTCGTAGCGCAACAGGG 1236

QY 928 AAGAAATCCGGTGCATGAACCCAACTACACAGACTTCAGATTCCCAAAATCAAGCCC 987
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Db 1237 AAGAAATTAATCATGAACCCAAATACACAGATTAGTTCCCAAAATCAAGCAC 1296
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QY 988 ACCCTTGGCATAAGGTTTTCCAAAGCGGATGCTCCGGAAGCCATTGACCTTGCATCTC 1047
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Db 1297 ACCATGGCAGAGATTATCCAAAGAGATGCCGAGAGCTGTTGATCTGCTCTC 1356
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QY 1048 GGCTTCTCAATCACTCACAAGTCTACGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1107
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QY 1108 TTTTCAATGAACCTCCGTGAGCCAAATGCTGCTTCCAAATGCGCACCTCTACCACTG 1167
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Db 1477 TATTCATTTCAAGC 1491
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RESULT 14
AV829186
LOCUS
DEFINITION AV829186 RAFL9 Arabidopsis thaliana cDNA clone RAFL09-40-M14 5',
mRNA sequence. EST. 594 bp mRNA linear EST 01-APR-2002
ACCESSION AV829186
VERSION AV829186.1 GI:19871246
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 594)
REFERENCE
AUTHORS Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M.,
Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y.
and Shinozaki, K.
TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998) cDNA cleaved with BamHI
and XhoI was ligated to modified lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
details.

FEATURES
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Matches 591; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DEFINITION OsIFCC011089 Oryza sativa Express Library Oryza sativa (indica
cultivar-group) genomic, genomic survey sequence.
ACCESSION CL964803.1 GI:52384296
VERSION
KEYWORDS
SOURCE Oryza sativa (indica cultivar-group)
ORGANISM Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartodeae; Oryzeae; Oryza.
1 (bases 1 to 2295)
REFERENCE
AUTHORS Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M.,
Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L.,
Wong, G.K.S., Deng, X.W. and Wang, J.
TITLE An analysis of transcriptional regulation of the rice genome and
its comparison to Arabidopsis
JOURNAL Unpublished (2004)
COMMENT Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
Location/Qualifiers

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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 05:27:02 ; Search time 12152.4 Seconds
(without alignment)
6929.914 Million cell updates/sec

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Perfect score: 1738
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: gb_hg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_ats.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	1565.6	90.1	1636	8	AY086529 Arabidops
4	1099.8	63.3	1143	6	CQ804868 Sequence
5	1099.8	63.3	1143	6	AX506180 Sequence
6	734.6	42.3	1636	8	ATASKDZET
7	733	42.2	1270	8	AY096698 Arabidops
8	733	42.2	1566	8	AY064020 Arabidops
9	733	42.2	1591	8	AY094423 Arabidops
10	732	42.1	1595	8	ATASKDNA
11	729.8	42.0	1503	8	AY087542 Arabidops
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19	666	38.3	1797	8	OSKETHA Y13437 Oryza sativ

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21	662.8	38.1	1818	8	AK105665	AK105665 Oryza sat
22	647.2	37.2	1744	8	BT009253	BT009253 Trifolium
23	647	37.2	1863	8	AK102147	AK102147 Oryza sat
24	613.4	35.3	1249	8	AY142595	AY142595 Arabidops
25	613.4	35.3	1634	8	AF428327	AF428327 Arabidops
26	613.4	35.3	1667	8	AY046024	AY046024 Arabidops
27	605.8	34.9	1592	8	AB059621	AB059621 Oryza sat
28	605.8	34.9	1717	8	AY085752	AY085752 Arabidops
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ALIGNMENTS

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LOCUS	A.thaliana mRNA for shaggy-like kinase etha.				
DEFINITION	X94939.1	GI:1161511			
ACCESSION	ASK etha gene, shaggy-like kinase etha.				
VERSION	Arabidopsis thaliana (thale cress)				
KEYWORDS	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
ORGANISM	Dornelas,M.C., Schwebel-Dugue,N., Thomas,M., Lechamy,A. and Kreis,M.				
REFERENCE	Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939 and X99696) (PGR97-008)				
AUTHORS	Plant Physiol. 113, 306-306 (1997)				
JOURNAL	2 (bases 1 to 1738)				
REFERENCE	Dornelas,M.C.				
AUTHORS	Direct Submission				
JOURNAL	Submitted (10-JAN-1996) M.C. Dornelas, UNIVERSITE de Paris-Sud, Institut de Biotechnologie des Plantes, Centre de Recherches sur les Plantes, URA 1128, Biol.du Devel.des Plantes, Bat.630, F-91405 ORSAY Cedex, FRANCE				
COMMENT	Corresponding genomic sequence is found in Y08947.				
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS

1 (bases 1 to 1670)
Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

TITLE
JOURNAL
AUTHORS

Arabidopsis cDNA clones
Unpublished
2 (bases 1 to 1670)
Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

TITLE
JOURNAL

Direct Submission
Submitted (25-JAN-2002) Salk Institute Genomic Analysis Laboratory (SIGAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Chang, E., Dale, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.

Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

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source

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DB	241	CCG	CCG
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DB	301	GAG	GAG
QY	391	AAA	AAA
DB	361	AAA	AAA
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VERSION	AY086529.1		
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ORGANISM	Arabidopsis thaliana		
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AUTHORS	Haas, B.J., Volkovsky, N., Town, C.D., Torkan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.		
TITLE	Full-length messenger RNA sequences greatly improve genome annotation		
JOURNAL	Genome Biol. 3 (6), RESEARCH0029 (2002)		
MEDLINE	22088475		
PUBMED	12093376		
REFERENCE	2 (bases 1 to 1636)		
AUTHORS	Brover, V., Torkan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.		
TITLE	Full-length cDNA from Arabidopsis thaliana		
JOURNAL	Unpublished		
REFERENCE	3 (bases 1 to 1636)		
AUTHORS	Brover, V., Torkan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.		
TITLE	Direct Submission		
JOURNAL	Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,		


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DEFINITION Sequence 875 from Patent WO0216655.
ACCESSION AX506180
VERSION AX506180.1 GI:23387417
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Harper, J.F., Kreps, J., Wang, X. and Zhu, T.
TITLE Stress-regulated genes of plants, transgenic plants containing same, and methods of use
JOURNAL Patent: WO 0216655-A 875 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG (CH)
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VERSION Y08947.1 GI:1627515
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ORGANISM Arabidopsis thaliana
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1
Dornelas, M.C. and Kreis, M.
Unpublished
REFERENCE 2 (bases 1 to 5985)
AUTHORS Dornelas, M.C.
TITLE Direct Submission
JOURNAL Submitted (18-OCT-1996) M.C. Dornelas, Universite de Paris Sud
(Paris XI), Institut de Biotechnologie des Plantes, Lab. Biol. du
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FRANCE
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 REFERENCE 1 (bases 1 to 1503)
 Haas, B.J., Volkovskiy, N., Town, C.D., Troughan, M., Alexandrov, N., Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L.
 Full-length messenger RNA sequences greatly improve genome annotation
 Genome Biol. 3 (6), RESEARCH0029 (2002)
 JOURNAL 22088475
 MEDLINE 12093376
 PUBMED
 REFERENCE 2 (bases 1 to 1503)
 Brover, V., Troughan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
 Full-length cDNA from Arabidopsis thaliana
 Unpublished
 JOURNAL
 REFERENCE 3 (bases 1 to 1503)
 Brover, V., Troughan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.
 Direct Submission
 Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA
 JOURNAL
 REFERENCE
 COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of

this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Genet carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.

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ORIGIN

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VERSION			
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DEFINITION	Arabidopsis thaliana putative shaggy kinase (Atlg06390) mRNA, complete cds.		
ACCESSION	AY051053	GI:15293238	
VERSION	AY051053.1		
KEYWORDS	FLI CDNA.		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE			
AUTHORS	Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Etnu, P., Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H., Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.		
TITLE	Arabidopsis Open Reading Frame (ORF) Clones		
JOURNAL	Unpublished		
AUTHORS	2 (bases 1 to 1255)		
	Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Banno, F., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S.E., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (02-AUG-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA		
COMMENT	The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.		
	The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Banno, F., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Tracy, S.E., Davis, R.W., Ecker, J.R. and Theologis, A.		

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

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	Db
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VERSION   AY035048.1 GI:14334749
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE   Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1582)
Yanada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,
Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Narusaka, M., Nguyen, M., Palm, C.J., Lam, B.,
Lin, J., Miranda, M., Shinn, P., Southwick, A., Shinozaki, K.,
Davis, R.W., Ecker, J.R. and Theologis, A.
Arabidopsis Full Length cDNA Clones
Unpublished
2 (bases 1 to 1582)
Yanada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,
Goldsmith, A.D., Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Yu, G.,

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Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y.,
Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M.,
Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M.,
Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and
Theologis, A.
Direct Submission
Submitted (03-MAY-2001) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
Arabidopsis Full-length cDNA'); Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.
The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Yamada, K., Liu, S.X.,
Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D.,
Lee, J.M., Quach, H.L., Tang, C.C., Toriumi, M., Yu, G., Bowser, L.,
Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koesema, E.,
Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J.,
Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
Yanada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to
this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC)
contributed equally to this work as PIs.
Annotation is based on the January 2002 version of the Arabidopsis
Genome submitted to GenBank.
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Best Local Similarity 76.6%; Pred. No. 1.1e-168;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
7547.973 Million cell updates/sec

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Scoring table: IDENTITY NUC
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Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: Geneseqn2000s:*
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- 12: Geneseqn2004as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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37	530.4	30.5	1429	5 AAH47003	Aah47003 Soy bean
38	530.4	30.5	1429	6 ABQ82533	Abq82533 Soybean g
39	519	29.9	1296	6 AB212869	Ab212869 Arabidops
40	519	29.9	1296	6 ADG87959	Adg87959 A. thalia
41	513.8	29.6	1654	8 ACC57971	Acc57971 Canola pr
42	513.8	29.6	1654	8 ACC57971	Acc57971 Canola pr
43	454.8	26.2	2787	10 AAL54220	Aal54220 Genomic D
44	454.8	26.2	2787	10 AAL54222	Aal54222 Mutant DN
45	444.4	25.6	458	6 ABL93707	Ab193707 Arabidops

ALIGNMENTS

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ID AAC47206 standard; DNA; 1745 BP.
XX AAC47206;
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DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52951.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
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 QY 1529 GTTGTATCGTTATTTCT 1588
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RESULT 3
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 XX AC AAC47997;
 XX DT 18-OCT-2000 (first entry)
 XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 55886.
 XX KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway; metabolic pathway;
 KW promoter; termination sequence; ss.
 XX OS Arabidopsis thaliana.
 XX PN EP1033405-A2.
 XX PD 06-SEP-2000.
 XX PF 25-FEB-2000; 2000EP-00301439.
 XX 25-FEB-1999; 99US-0121825P.
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Qy 792 ATTCTTACATCTGCTCAGATTTCTACCGTGCAACCGAGCTCATATTTGGTGCACTGAG 851
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Qy 852 TACACAACTTATTCATATCTGTTCTGCTGCTGTTGTTCTTGCTGAGCTTCTTCTTGGT 911
Db 786 TACACAACTTCCATGATATTTGGTCTGCTGTTGTTCTGCTGAGCTTCTTCTTGGT 845
Qy 912 CAGCCATTATTCCTCCGAGAAAATGCTGTGGATCAGCTCGTGGAATTTATAAGTTCTT 971
Db 846 CAGCCATTATTCCTCGAGAAAATGCTGTGGTCAGCTCGTTGAATTCATCAAGTTCTT 905
Qy 972 GGTACACCAACTCGAAGAAATTCGTTGTATGAATCCCAACTPACACAGATTTCAAGTTC 1031
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ID AAC47571 standard; DNA; 1501 BP.
XX
AC AAC47571;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 54312.
DE
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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Db 504 AGAGACATTTGACCGGTTTGAAGCACTATAGTATCAAAACAGCGGATGCTATCTT 563
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Db 564 CTATGTTCAACTTTACATACCAATCTTCAGAGGCTTGGCTTATATCCATCTGCTCC 623
Qy 677 GGGAGTTTGTACAGAGATCTAAAGCCTCAAAATCTTCTGGTTGATCCTCTTACTCATCA 736
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Qy 737 AGTCAAAATCTGTGACTTTGGGAGTGGGAAACAGCTCGTTAAAGGTGAACCAAAATTC 796
Db 684 GTGTAAGCTCTGTGATTTTGAAGTGAAGAGTACTGTGTGAAAGGTGAAGCAAAATATC 743
Qy 797 TTAATCTCTGCTACGATTTCTACCGTGCACCCGAGCTCATATTTGGTGGCACTGAGTAC 856
Db 744 ATATATCTGCTCTCGGTATTTACCGAGCTCCAGAACTCATCTTTGGTGGCAGAGTATAC 803
Qy 857 AACTTCTATGATATCTGCTCTGCTGTTGTGTTCTTGTGAGCTTCTTCTTGGTCAGCC 916
Db 804 ATCAATCAATGATATGCTGCTGCTGTTGTTCTTGGCAGAGCTACTTCTTGGGAGCC 863
Qy 917 ATTATTTCCCGGAGAAATCTGTGATCAGCTCGTGGGAAATTTATTAAGTTCTTGGTAC 976
Db 864 GTTATTTCCCGGAGAAATTTCTGTGACCAAGTGTGATGATCAAAAGGTTCTTGGTAC 923
Qy 977 ACCAACTCGAGAGAAATCGTTGTATGAATCCCACTACACAGATTTCAAGTTCCCA 1036
Db 924 TCCAACTCGGAGAGAAATCCGGTGCATGAACCCAACTACACAGATTTCAAGTTCCCA 983
Qy 1037 GATAAGGCCCATCTCCCTGGCACAAGATCTTTCCAAAGGATGCCCCCAAGCGGTTGA 1096
Db 984 AATCAAGCCCACTTGGCATAGGTTTTCACAAAGCGGATGCTCCCGAAGCCATTGA 1043
Qy 1097 TTTGGCATCAAGGCTGTTCAATCTCTCAAGTCTAAGATGACACAGCGCTCGAAGCTTG 1156
Db 1044 CTTGCACTCTCGGCTTCTTCAATCTCTCACTACCAAGTCTACGTTGCACTGCGCTCGAGCATG 1103
Qy 1157 TGCAATCCGTTCTTTGATGAATCTCAGAGAACCAAGCGTCTGTTTACCAATCGAGCGCC 1216
Db 1104 TGGCATCTCGGTTTTCATGAATCTCGTGAAGCAATGCTGCTTCCAAATGGCGACC 1163
Qy 1217 TCTCCCGCTCTCTTCAACTTTCAACCAAGAGTGTGATCATCATCTGAACTGGTCAA 1276
Db 1164 TCTACCACTGTTGTTCACTTTCAACCAAGAGTTGCTCTGGGGCTTCCCGAGCTTATCAA 1223
Qy 1277 CAAGTTGATTTCCAGACATATCAAGAGCAATTTGGGCTTAAGCTTCTTGAATCAATCTGG 1336
Db 1224 CAGGTAATACAGAGATGTGAGCGCACAGATGAATGTGGCTTTTCCATTTCAAGCTGG 1283
Qy 1337 AACTTAAAA 1345
Db 1284 ACCCTAGAA 1292

RESULT 9
AAC37569
ID AAC37569 standard; DNA; 1503 BP.
XX
AC AAC37569;
XX

DT 17-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 17866.
DE Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
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PR 24-MAY-1999; 99US-0135629P.
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PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
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PR 18-JUN-1999; 99US-0139459P.
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PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.

Db 386 CCGAGAGTGGCAATTAATGCGACTAATGGACCAATCAAAATGTGGTTTCTTGAAGCATTTG 445
 Qy 497 CTTCTTTTTCGACTACAGAGAAACAGAGCTTTTCTTGAACCTTGGTTATGGAGTATGTCC 556
 Db 446 TTTCTTTCTTACAAACGACTAGAGATGAGCTTCTCTCAATCTCGTTATGGAGTATGTACC 505
 Qy 557 TGAGAGCTTGTATCTGAGTCTTGAAACATATATAGTAGTGCAAAACCAAGAAATGCTCTTGT 616
 Db 506 AGAGACATTTGACCGGTTTGAAGCACTATATAGTTCAAAACGCGGATGCTATCTT 565
 Qy 617 CTATGTTAACTTTTACAGTATCAGATCTTCGGGAGCTTGTCTTCAATCAACAGTTGCC 676
 Db 566 CTATGTCAAACCTTTACACATACCAATCTTCAGAGGCTTGGCTTATATCCATCTGCTCC 625
 Qy 677 GGGAGTTTGTACAGAGATCTAAGCTCAAACTCTTCTGTTGATCTCTTACTCATCA 736
 Db 626 TGGTGTCTGCCACAGAGATGTGAACCACAAAATCTTTTGGTTGATCCCTTACCCATCA 685
 Qy 737 AGTCAAAATCTGTGACTTTTGGCAGTGCMAACAGCTCGTTAAAGGTGAACCAAACTTTC 796
 Db 686 GTGTAGCTCTGTGATTTTGAAGTGCMAAAGTACTGTGCAAGGTGAAGCAACATATC 745
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 Db 746 ATATATCTGCTCTCGGTATTTACCGATCTCCAGAACTCATCTTTGGTGCACAGAGTATAC 805
 Qy 857 AACTTCTTATGATCTGGTCTGCTGGTGTGTCTTCTGCTGAGCTTCTTCTTGGTCAACC 916
 Db 806 ATCATCATTTGATATGCTGCTGCTGGTGTGTCTTGGCAGAGCTACTTCTTGGGAGCC 865
 Qy 917 ATTATTTCCCGGAGAAATCTCTGGATCAGCTCGTGGMAATTTATAAGTCTTCTGGTAC 976
 Db 866 GTTATTTCCCGGAGAAATCTCTGGACCGCTAGTGGAGATCATTAAGTCTTCTGGTAC 925
 Qy 977 ACCAACTCGAGAGAAATCCGTTGTATGAATCCCACTACAGATTTCAAGTTCCCA 1036
 Db 926 TCCAACTCGGAGAAATCCGTTGTATGAATCCCACTACAGATTTCAAGTTCCCA 985
 Qy 1037 GATAAGGCCATCCCTGGCACAGATCTTCCCAAAAGAGTCCCGGAGGCTTGA 1096
 Db 986 AATCAAGGCCATCCCTGGCATAGGTTTCCCAAGCGGATGCTCCCGAAGCCATTGA 1045
 Qy 1097 TTTGGCATCAAGGCTGCTCAATCTCTCAAGTCTAAGATGCACAGCGCTCGAAGCTTG 1156
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 Qy 1157 TGCAATCTCGTCTTTGATGAATCTCAGAGAACCAACGCTCGTTTACCAATGGAGGCC 1216
 Db 1106 TGGCATCCGCTTTTCAATGAACTCCGCTGAGCCAAATGCTCGTCTTCCAAATGGCGACC 1165
 Qy 1217 TCTCCGCTCTCTTCAACTTCAACAGAGTACGCTGGATCATCACCTGAATGGTCAA 1276
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 Qy 1337 AACTTAAAA 1345
 Db 1286 ACCCTAGAA 1294

RESULT 10

ACC57975
 ID ACC57975 standard; cdna; 1744 BP.

AC

XX

AC

XX

XX

DT

11-AUG-2003 (first entry)

XX

DE

XX

Soybean protein kinase stress-related polypeptide GmPK-3 cdna.

KW GmPK-3; protein kinase stress-related polypeptide; PKSRP; enzyme;
 KW transgenic plant; plant; stress tolerance; drought tolerance;
 XX salt tolerance; cold tolerance; soybean; gene; ss.
 OS Glycine max.
 XX
 FH Key Location/Qualifiers
 FT CDS 40..1302
 FT /*tag= a "GmPK-3"
 FT /product= "GmPK-3"
 XX
 PN WO2003040171-A2.
 XX
 PD 15-MAY-2003.
 XX
 XX 12-NOV-2002; 2002WO-US036374.
 PF
 XX 09-NOV-2001; 2001US-0346096P.
 PR
 XX (BADI) BASF PLANT SCI GMBH.
 PA
 XX Van Thiel N, Da Costa E SilvaO, Chen R;
 PI WPI; 2003-441522/41.
 XX DR P-PSDB; ABR42368.
 DR
 XX
 PT New protein kinase stress-related polypeptide coding nucleic acid, useful
 PT for producing transgenic plants with an increased tolerance to an
 PT environmental stress, e.g. high salinity, as compared to a wild type
 PT variety of the plant.
 XX
 XX Claim 1; Page 96-97; 111pp; English.
 PS
 XX The present sequence is a full-length cDNA encoding GmPK-3, a novel
 CC soybean protein kinase stress-related polypeptide (PKSRP). The cDNA was
 CC identified on the basis of homology to Physcomitrella patens PK-3 (see
 CC ACC57962) and PK-10 (see ACC57966) sequence. GmPK-3 is an example of
 CC PKSRPs of the invention that are important for modulating a plant's
 CC response to environmental stress. Over-expression of PKSRP coding nucleic
 CC acids in a plant results in the plant's increased tolerance to
 CC environmental stress. Transgenic monocot and dicot plants are provided
 CC that show increased tolerance to high salinity, drought and low
 CC temperature
 XX
 SQ Sequence 1744 BP; 502 A; 379 C; 380 G; 483 T; 0 U; 0 Other;
 Query Match 41.7%; Score 724; DB 8; Length 1744;
 Best Local Similarity 74.8%; Pred. No. 3.9e-191;
 Matches 907; Conservative 0; Mismatches 305; Indels 0; Gaps 0;
 Qy 197 CGCCATGGCTGATGATAAGGAGATGCTGCTGTGTAGTTGATGGACATGATCAAGTCAC 256
 Db 156 CGATGTGGAGACCGATPAGATATATGTCAGTACTGTCATTTGAGGGGAATGATGCTGTAC 215
 Qy 257 TGGTCTATATTATTTCCACCACCAATCGGTGGCAAAAAATGGTGAACCAAAAAACAGCAATTAG 316
 Db 216 TGGCCACATAATCTCCACCACCAATTTGGAGGCAAAAAATGGGAACCTTAAAGAGACCATCAG 275
 Qy 317 TTACATGGCGGAGCGAGTTGTTGGTACAGGCTGTTCCGGATCGTTTCCAGCAAAATG 376
 Db 276 TTACATGGCAGAACGTTGTTGGTGGCACTGGATCATTTGGAGTTGTTTTCAGGCAAGTG 335
 Qy 377 TTTGGAGACTGGAGAAACCGTGGCGGATAAAGAGGTTTTCAGAGATAGAGATACAGAA 436
 Db 336 CTTGGAGACTGGAGAGCAGTGGCTATTAAAGGCTTTCAGACAGACGCGGTACAAAA 395
 Qy 437 CCAGAACTTTCAGTTGATGCTGTGATGATCATCCGAATGTTGTTTGAAGCATTC 496
 Db 396 TCGTGAATTGCACTTAATGCGCTTAATGGATCACCCCTTAATGTAATTTCCCTGAAGCACTG 455
 Qy 497 CTTCTTTTTCGACTACAGAGAAACAGAGCTTTTCTTGAACCTGTTTATGGAGTATGCCC 556
 Db 456 TTTCTTTCTCCACAACAGCAGAGATGAACCTTTTCTTAAACCTTGGTAATGAATATGTTCC 515

PR	08-JUL-1999;	99US-0142803P.	PR	24-SEP-1999;	99US-0155659P.
PR	09-JUL-1999;	99US-0142320P.	PR	28-SEP-1999;	99US-0156458P.
PR	12-JUL-1999;	99US-0142377P.	PR	29-SEP-1999;	99US-0156596P.
PR	13-JUL-1999;	99US-0143342P.	PR	04-OCT-1999;	99US-0157117P.
PR	14-JUL-1999;	99US-0143624P.	PR	05-OCT-1999;	99US-0157533P.
PR	15-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.
PR	16-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158029P.
PR	16-JUL-1999;	99US-0144086P.	PR	08-OCT-1999;	99US-0158232P.
PR	19-JUL-1999;	99US-0144325P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0158293P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159329P.
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PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159637P.
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PR	21-JUL-1999;	99US-0144814P.	PR	14-OCT-1999;	99US-0159584P.
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PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.
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PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.
PR	27-JUL-1999;	99US-0145919P.	PR	26-OCT-1999;	99US-0161359P.
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PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-0161920P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161922P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161993P.
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PR	01-SEP-1999;	99US-0151930P.			
PR	07-SEP-1999;	99US-0152363P.			
PR	10-SEP-1999;	99US-0153070P.			
PR	13-SEP-1999;	99US-0153758P.			
PR	15-SEP-1999;	99US-0154018P.			
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Query Match 38.9%; Score 676.8; DB 3; Length 1653;

Best Local Similarity 75.3%; Pred. No. 5.8e-178; Indels 0; Gaps 0;

Matches 843; Conservative 0; Mismatches 277; Indels 0; Gaps 0;

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DB	228	GAGGGAAGAAATGGAGAGCCTAAAGGACTATCAGCTACATGGCAGAGAGATTGTGGAA	287
QY	343	CAGGCTCGTTCCGGATCGTTTTCCAGCAAAATGTTTGAGACTGCGAGAAACCGTGGCGA	402
DB	288	CTGGATCATTTGGAATCGTCTCCAGGCAAAATGCTGGAGACTGGTGAGACTGTGGCGA	347
QY	403	TAAAGAAGGTTTTGCAAGATAGAAGATACAAGAACCGAGAATTCAGTTGATCGGTGA	462
DB	348	TTAAGAAGGTTTTGCAGGCAAGCGCTACAAGACAGGAGCTACAAATCATCGGATCCA	407
QY	463	TGGATCATCCGAATGTGGTTTTGTTGAAGCATTTGCTTTTCGACTACAGAGAAAGACG	522
DB	408	TGGATCACTGCAATGTGTTTCTCCCTGAAGCATTTGCTTTCTTACCAAGCAGAGATG	467
QY	523	AGCTTTCTTGAACCTTGGTTATGGAGTATGTCCTGAGAGCTTGTATCGAGTTCTGAAAC	582
DB	468	AACCTTTCTTAACTTAGTGTAGTGAGTTGTTCCCGAGTCATTATATCGGTTGTAAC	527
QY	583	ATTATAGTAGTGCAAAACCAAGAAATGCCCTCTTGTCTATGTTAACTTTTACAGTTATCAGA	642
DB	528	ATTACAGCAATATGAACCAAGAGATGCCACTCATTTATGTCAAAATATATATACCTACAGA	587
QY	643	TCCTCCGGGAGCTTGGTTACATTCACAGTTGCCGGGAGTTTGTCTACAGAGATCTAAGC	702
DB	588	TATTTCCAGGCTTAGCCTATATTACACAGTAGTACCTGGAGTTTTCACCAAGGATGTGAAAC	647

Qy	957	ATTATTAAGTTC	TTGGTACACCAACTCGAAGAAATCCGTTGTATGAATCCCAACTAC	1016
Db	869	ATTATCAAGGTTCT	TTGGTACTCCAAACCGGTGAGGAAATTCGGTGCATGAACCCCAACTAT	938
Qy	1017	ACAGATTCAAGTTCC	CACAGATAAAGGCCCATCCCTGGCACAGAATCTTCCACAAAGG	1076
Db	929	ACCGAGTTCAAGTTCT	CTCAGATTAAAGGCTCATCTTTGGCACAGAATTTTCCACAAAGAGA	988
Qy	1077	ATGCCCCAGAAAGCG	TTTGATTTGGCATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGA	1136
Db	989	ATGCCCCGTGAAGCT	ATAGATCTTGCCCTCCGCTTCTCCAGTATTCACCAATCTACGT	1048
Qy	1137	TGCACAGCGCTCGA	AGCTTGTGACATCCGTTCTTTGATGAACCTCAGAGAACCAACGCT	1196
Db	1049	TGCACTGCTCTTGAT	GCATGTGCACATTCCTTCTTGATGAGCTACGTGAGCCGATGCA	1108
Qy	1197	CGTTTACCAATGCA	CGCGCTCTCCCGCTCTCTTCAACTTCAACGAAGTAGCTGA	1256
Db	1109	CGCTTGGCGAATG	CGCCCATTCCTCTCTGTTCAACTTCAACCTGAACCTAGCGAAC	1168
Qy	1257	TCATCACTGAAC	TGGTCAACAAGTGTGATTTCCAGACCATATCAAGACAAATTTGGGTCTA	1316
Db	1169	GCCTTCTCAGAG	CTCATCAAGGCTGTTCCGGGAACATGTTCCAGCGGAAAATGGCCCC	1228
Qy	1317	AGCTTC	1322	
Db	1229	AAC TTC	1234	
RESULT 15				
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ID	AB082534 standard; cDNA; 1673 BP.			
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AC	AB082534;			
XX				
DT	19-DEC-2002 (first entry)			
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DE	Wheat glycogen synthase kinase encoding cDNA SEQ ID NO:15.			
XX				
KW	Glycogen synthase kinase; kinase; enzyme; plant; immunological screening;			
KW	plant breeding; gene; ss.			
OS	Triticum aestivum.			
XX				
XX				
Key	Location/Qualifiers			
FT	44..1252			
FT	/*tag= a			
FT	/product= "glycogen synthase kinase"			
XX				
XX				
PN	US2002120949-A1.			
XX				
PD	29-AUG-2002.			
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XX	14-MAY-2001; 2001US-00854731.			
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PR	10-JUL-1998; 98US-0092438P.			
PR	02-JUL-1999; 99US-00347801.			
XX				
PA	(ALLE/) ALLEN S M.			
XX				
PI	Allen SM;			
XX				
DR	WPI; 2002-731384/79.			
DR	P-PSDB; ABP53636.			
XX				
PT	New calcium-dependent phosphorylase kinase and glycogen synthase kinase			
PT	polypeptides, for altering level of expression of kinase polypeptides in			
PT	plants.			
XX				
PS	Claim 15; Page 22-24; 4lpp; English.			
XX				
CC	The present invention describes kinase polypeptides (I) such as a calcium			

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	734.6	42.3	1636	4	US-09-578-194-6	Sequence 6, Appli
2	649.2	37.4	1673	3	US-09-347-801-15	Sequence 15, Appl
3	649.2	37.4	1673	4	US-09-854-731-15	Sequence 15, Appl
4	590	33.9	1814	3	US-09-347-801-9	Sequence 9, Appli
5	590	33.9	1814	4	US-09-854-731-9	Sequence 9, Appli
6	530.4	30.5	1429	3	US-09-347-801-13	Sequence 13, Appl
7	530.4	30.5	1429	4	US-09-854-731-13	Sequence 13, Appl
8	389.6	23.0	1952	4	US-09-566-921-24	Sequence 24, Appl
9	399.6	23.0	2154	3	US-09-488-856A-3	Sequence 3, Appli
10	393.2	22.6	2088	2	US-08-602-264A-1	Sequence 1, Appli
11	393.2	22.6	2088	3	US-08-461-018A-1	Sequence 1, Appli
12	393.2	22.6	2088	3	US-09-216-958-1	Sequence 1, Appli
13	391.6	22.5	1389	3	US-09-489-765A-3	Sequence 3, Appli
14	391.6	22.5	1389	4	US-09-016-434-1414	Sequence 3, Appli
15	391	22.5	1972	2	US-08-602-264A-2	Sequence 2, Appli
16	391	22.5	1972	3	US-08-461-018A-2	Sequence 2, Appli
17	391	22.5	1972	3	US-09-216-958-2	Sequence 2, Appli
18	286.4	16.5	1185	4	US-09-248-796A-4396	Sequence 4396, Ap
19	163	9.4	304	4	US-09-313-294A-6825	Sequence 6825, Ap
20	142.4	8.2	305	4	US-09-313-294A-6825	Sequence 5874, Ap
21	142.2	8.2	286	4	US-09-313-294A-2895	Sequence 2895, Ap
22	129.8	7.5	1236	4	US-09-248-796A-4397	Sequence 4397, Ap
23	115.6	6.7	272	4	US-09-313-294A-6721	Sequence 6721, Ap
24	107	6.2	584	3	US-09-347-801-11	Sequence 11, Appl
25	107	6.2	584	4	US-09-854-731-11	Sequence 11, Appl
26	106.4	6.1	275	4	US-09-313-294A-1703	Sequence 1703, Ap
27	101	5.8	479	2	US-08-602-264A-13	Sequence 13, Appl

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QY 317 TTACATGCGGAGCGAGTTGTTGGTACAGCTCGTTTCGGGATCGTTTTCACAGCAAAATG 376
DB 257 TTACATGCGGAGCGAGTTGTTGGTACAGCTCGTTTTCGGGATCGTTTTCACAGCAAAATG 316
QY 377 TTTGGAGACTGGAGAAACCGTGCGGATGAAGAGTTTTCGAGATGAGAGATACAGAA 436
DB 317 CTTGGAACTGGAGAACTAGTAGCCATTAAGAGGTTTTCGAGATGCGCGTTATATAAA 376
QY 437 CCGAGAACTTCAGTTGATCGGTGATGATCATCCGAATGTTGTTGTTGAAGCAATG 496
DB 377 CCGAGAGTTGCAATTAATCGCACTAATGACCATCCAAATGTTGTTTCCCTGAAGCAATG 436
QY 497 CTTCTTTTCGACTACAGAGAAACAGCAGCTTTTCTTGAACCTGTTGTTATGAGTATGTC 556
DB 437 TTTCTTCTCTACACGACTAGATGAGCTTCTCTCAATCTCGTTATGAGATGATGACC 496
QY 557 TGAGAGCTTGTATCGAGTTCTGAAACATTAATAGTAGTGCAAAACCAAGAAATGCTCTTGT 616
DB 497 AGAGACATTTGACCGGTTTGAAGCACTATACCTAGTTCAAACGAGCGATGCTATCTT 556
QY 617 CTATGTTAACTTTACAGTTATCAGATCTTCCGGGACTTGTCTTACATTCACAGTTGCC 676
DB 557 CTATGTTAACTTTACACATACCAAACTCTTCAGAGGCTTGGCTTATATCCATCTGCTCC 616
QY 677 GCGAGTTTGTACAGAGATCTAAGGCTCAAAATCTTCTGTTGATCTCTTACTCATCA 736
DB 617 TGGTGTCTGCCACAGAGATATAAAACACAAATCTTTTGGTTGATCCCAACACCATCA 676
QY 737 AGTCAAAATCTGTGACTTTGGCAGTCGAAACAGCTCGTTAAAGGTGAACCAAACTTTC 796
DB 677 GTGTAAGCTCTGTGATTTTGAAGTGAAGAGTACTGTTGTAAGGTGAACCAAACTATC 736
QY 797 TTACATCTGCTACGATTTCTACCGTGCAACCGAGCTCATATTTGTTGCTGAGTAC 856
DB 737 ATATATCTGCTCTCGGTATTTACCGAGCTCCAGAACTCATCTTTGTTGTCACAGAGTATAC 796
QY 857 AACTCTTATGATATCTGTTCTGCTGTTGTTGTTCTGAGTCTTCTTCTTGGTCAAGC 916
DB 797 ATCATCATTTGATATATGTTCTGCTGTTGTTCTGCGAGACTACTTCTTGGGAGAGC 856
QY 917 ATTATTTCCCGGAGAAATCTGTGGATCAGCTCGTGGAAATTAATTAAGTTCTTGGTAC 976
DB 857 GTTATTTCCCGGAGAAATTTCTGTGACAGCTAGTGGAGATCATAAAGTTCTTGTGATAC 916
QY 977 ACCAATCTCGAGAGAAATCTGTTGATGATATCCAACTACACAGATTTCAAGTTTCCACA 1036
DB 917 TCCAACTCGCGAGAAATCCGTTGATGATGAACCCAACTACACAGATTTCCAGATTTCCACA 976
QY 1037 GATAAAGGCCCCCTCGGCACAGATCTTCCACAAAGGATGCCCCCGAGAGCGGTGCA 1096
DB 977 AATCAAGCCCCCTTGGCATTAAGTTTTCACAAAGCGATGCCCTCCGAGAGCAATGA 1036
QY 1097 TTTGGCATCAAGCTGCTCTTCAATCTCTCAAGTCTAAGATGACAGCGCTCGAAGCTTG 1156
DB 1037 CCTTGATCTCGGCTTCTTCAATCTCACCAGTCTACGTTGACATGCGCTCGAGGCATG 1096
QY 1157 TGACATCTCGTCTTCTTGAATGAACTCAGAGAACCAAGCTCGTTTACCAATGAGCGGC 1216
DB 1097 TGGCATCTCGGCTTCTTCAATCTCACCAGTCTACGTTGACATGCGCTCGAGGCATG 1156
QY 1217 TCTCCGCGCTCTCTCAACTTCAAAACAAAGAGTACGTGGATCATCACTGAACTGTGCA 1276
DB 1157 TCTACACCGCTGTTCTCACTTCAACAGAGTTGCTGCGGCTTACCGAGGCTTATCAA 1216
QY 1277 CAAGTTGATTCAGACCATATCAAGAGCAATTTGGGTCTAAGCTTCTTGAATCAATCTGG 1336
DB 1217 CAGGCTAATACAGAGCATGTGAGGCGACAGATGAATGGTGGCTTTCCATTTCAAGCTGG 1276
QY 1337 AACTTAAAA 1345
DB 1277 ACCCTAGAA 1285

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RESULT 2
US-09-347-801-15
; Sequence 15, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1349)
US-09-347-801-15

Query Match      37.4%; Score 649.2; DB 3; Length 1673;
Best Local Similarity 74.9%; Pred No. 2.4e-175;
Matches 813; Conservative 0; Mismatches 273; Indels 0; Gaps 0;

QY 237 GATGGACATGATCAAGTCATCTGTCATATATTTCCACACAAATCGTGGCAAAATGTG 296
DB 149 GAGGGGAACGACGCCATGACCGGTACATCATCTCCACCACCATCGCGCGCAAGAACGCG 208
QY 297 GAACCAAAACACACAATTAGTTACATGCGGGAGCGAGTTGTTGGTACAGGCTCGTTCGG 356
DB 209 GAGCCCAAGCAGACGATTAGCTACATGCGCGAGCGGTTGTGGGCACCTGTTGCTTTGCG 268
QY 357 ATCGTTTTCACAGCAAAATGTTTGGAGACTGGAGAAACCGTGGCGGATATAAGAGGTTTGG 416
DB 269 ATCGTCTTTCAGCTTAATGCTCGAACCAGGAGAGTGTGGGCATTAAGAGGTTACTG 328
QY 417 CAAGATAGAGATACAAAGAACCGAGAACTTCAGTTGATGTCGTTGATGATCATCCGAAT 476
DB 329 CAGGACAGCGGTACAAAGAACCGTGAAGTTCAGCTGATGATGATGATGATGATGATGAT 388
QY 477 GTGGTTTGTTCAGCAATGCTTCTTTTCGACTACAGAGAAACGAGCTTTTCTTGTGAAC 536
DB 389 GTTGTCTCCTCAAGCAGCTGCTTCTTCAACCAAGTAGAGATGAGCTGTTCTCTGAAC 448
QY 537 TTGGTTTATCGAGTATGTCCTCGAGAGCTGTTGATCGAGTTCTGAAACATTTATAGTAGTGA 596
DB 449 CTTGTATGAGATGATGTCCTCGAGAGCGCTATACCGGCTGCTTAAGCAGCTACAGTATGCC 508
QY 597 AACCAAGAAATCGCTTCTGTTGTTAACTTTTACAGTTATCAGATCTTCGGGGAGCTT 656
DB 509 AACCGGGGATGCGGCTTATCTATGTCAGCTTTTACATGATCAGCTTTTATAGAGGCTA 568
QY 657 GCTTACATTCAGAGTTGCGGGAGTTTGTACAGAGATCTAAAGCTCAAAATCTTCTG 716
DB 569 GCTTATGTTTCACTGTTTCCAGGAGTTTCCACAGGAGTGTGAACCAACAAATGTTTGTG 628
QY 717 GTTGTATCTCTTACTCATCAAGTCAAAATCTGTGACTTTTGGCAGTGGCAAAACAGCTCGT 776
DB 629 GTTGTATCTCTTAACCCATCAAGTCAAGATCTGTGACTTTTGGAGTGCAGAAAGTTCTGTA 688
QY 777 AAAGGTGAACCAAAACATTTTTCATCTGCTCAAGATCTACCGTGCAACCGAGCTCAT 836
DB 689 CTTGGTGAACCAACATAGCATACATATGCTCTCGTACTATCTGCTCTCTGAGCTCAT 748
QY 837 TTTGGTGGCAGTACAGTACAACTTCTTATGATATCTGCTGCTGCTGCTGCTGCTGCT 896
DB 749 TTTGGTGAACCTGAATATACAACTTCAATAGACATATGCTGAGCTGATGTTGTTCTTGCA 808

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QY 897 GAGCTTCTTCTGGTCAAGCATTATTTCCCGGAGAAATGCTGTGATCAGCTCGTGGAA 956
DB 809 GAGCTACTTCTTGGTCAAGCCTCTGTTTCCAGAGAGACTGCGGTGATCAGCTAGTGGAG 868
QY 957 ATTATTAAGTTCTTGGTACACCACTCGAGAGAAATCCGTTGTATGAATCCCAACTAC 1016
DB 869 ATTATCAAGTTCTTGGTACTCCAACTCGAGAGAAATTCGGTGCATGAACCCCACTAT 928
QY 1017 ACAGATTTCAAGTTCCCAAGATTAAGGCCATCCCTGGCACAAGATCTTCCACAAAAGG 1076
DB 929 ACCGAGTTCAAGTTCTTCCAGATTAAGGCTCATCTTGGCACAAGATTTTCCACAAGAGA 988
QY 1077 ATGCCCCCAAGAGCGGTGATTTGGCATCAAGCGTCTTCAATCTCTCCAGTCTTAAGA 1136
DB 989 ATGCCCGCTGAAGCTATAGATCTTCCCTCCCGCTTCTCCAGTATTCACCAATCTAGCT 1048
QY 1137 TGCACAGCGCTCGAAGCTTGTGCACATCGTTCTTTTGTGAATCAGAGAACCAACGCT 1196
DB 1049 TGCACCTGCTTGTATGATGTCACATTCCTTCTTGTGATGAGCTAGCTGAGCCGAATGA 1108
QY 1197 CATTACCAATGGAGCGGCTCTCCGGCTCTCTTCAACTTCAAAACAAGATAGCTGGA 1256
DB 1109 CGCTTGCAGATGGCGGCCATTTCCCTCTCTGTTCAACTTCAAACTTCAAACTAGCGAAG 1168
QY 1257 TCATCAGCTGAAGCTGTCACCAAGTTGATTCAGACCATATCAAGAGACAAATGGGTCTA 1316
DB 1169 GCCTCTCAGAGCTCATCAACAGGCTTGTTCGGGAACATGTTTCGACGGCAAAATGGCCCC 1228
QY 1317 AGCTTC 1322
DB 1229 AACTTC 1234

RESULT 3

US-09-854-731-15
; Sequence 15, Application US/09854731
; Patent No. 6794561
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: *Triticum aestivum*
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1349)
US-09-854-731-15

Query Match 37.4%; Score 649.2; DB 4; Length 1673;
Best Local Similarity 74.9%; Pred No. 2.4e-175;
Matches 813; Conservative 0; Mismatches 273; Indels 0; Gaps 0;
QY 237 GATGACATGATCAAGTCACTGGTCATATTAATTTCCACCACATCGGTGGCAAAATGTT 296
DB 149 GAGGGGAACGACGCCATGACCGGTCACTATCTCCACCACCATCGCGGCAAGAACGGC 208
QY 297 GAACCAACACAGACAAATAGTTACATGCGGAGCGAGTGTGGTACAGGCTCGTTCGG 356
DB 209 GAGCCCAAGCAGACATAGCTACATGCGGAGCGCGTGTGGGCACTGGTTCTGTTTGGC 268
QY 357 ATCGTTTTCCAGCAAAATGTTTGGAGACTGGAGAAACCGTGGCGCATAAAGAGGTTTG 416
DB 269 ATCGCTTTTCAAGCTTAATGCTTGGAAACCGGGGAGATGTTGGGCAATTAAGAGGTACTG 328

RESULT 4

US-09-347-801-9
; Sequence 9, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases

QY 417 CAAGATAGAAGATCAAGAACCGGAACTTCAGTTGATCGTGTGATGGATCATCCGAT 476
DB 329 CAGGACAGACGGTCAAGAACCGTGAGCTGCAGCTTATGCGTTGATGATCATTCCTCAAT 388
QY 477 GTGGTTCTTGTGAAGCATTTGCTTCTTTTCGACTACAGAGAAAGAGAGCTTTCTTTGAAC 536
DB 389 GTTGTCTCCCTCAAGCACTGCTTCTTCTCAACCAAGTAGAGATGAGCTGTTCTCTGAAC 448
QY 537 TTGGTTATGAGATGTCCTCCCTGAGACGTTGTATCGAGTTCTGAAAACATTAATAGTAGTGA 596
DB 449 CTTGTCAATGAGATGTCCTCCGAGACGCTATACCCGCTGCTTAAGCACTACAGTAATGCC 508
QY 597 AACCAAGAAATGCCCTCTGCTATGTTTAAATTTTACAGTTATCAGATCTTCCGGGACTT 556
DB 509 AACCAAGGGAATGCCGCTTATCTATGTCAAGCTTTTACATGTATCAGCTTTTATAGAGGCT 568
QY 657 GCTTACATTCACAGTTGCGCGGAGTTTGTCAACAGATCTAAAGCCTCAAAATCTTCTG 716
DB 569 GCTTATGTTTCACTGTTTCCAGGAGTTTGCACAGGATGTGAACACCAAAATGTTTGG 628
QY 717 GTTGATCTCTTACTCATCAAGTCAAAATCTGTGACTTTGGCAGTGGCAAAACAGCTCGTT 776
DB 629 GTTGATCTCTTAAACCAATCAAGTCAAGATCTGTGACTTTGGAAGTGCAAAAGTTCTGGTA 688
QY 777 AAAGTGAACCAACAAATTTCTTACATCTGCTCAAGATCTACCGTGCACCCGAGCTCAT 836
DB 689 CTTGTGAACCAACCAATAGCATACATATGCTCTCGCTACTATCTGCTCTCTGAGCTCAT 748
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DB 809 GAGCTACTTCTTGGTCAAGCTCTGTTTCCAGAGAGACTGCGGTTGATCAGCTAGTGGAG 868
QY 957 ATTATTAAGTTCTTGGTACACCAACTCGAGAGAAATCCGTTGTATGAATCCCAACTAC 1016
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QY 1017 ACAGATTTCAAGTTTCCCAAGATTAAGGCCCATCCCTCGGCAACAGATCTTCCACAAAAGG 1076
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DB 989 ATGCCCGCTGAAGCTATAGATCTTGGCTCCCGCTTCTCCAGTATTCACCAATCTAGCT 1048
QY 1137 TGCACAGCGCTCGAAGCTTGTGCACATCGGTCTTGTGATGAATCAGAGAACCAACGCT 1196
DB 1049 TGCACCTGCTTGTATGATGTCACATTCCTTCTTGTGATGAGCTAGCTGAGCCGAATGA 1108
QY 1197 GCTTACCAATGAGACGGCTCTCCCGCTCTTCAACTTCAAAACAAGATAGTCTGGA 1256
DB 1109 CGCTTGCAGAAATGGCGGCCATTTCCCTCTCTGTTCAACTTCAAACTTCAAACTAGCGAAG 1168
QY 1257 TCATCAGCTGAAGCTGTCACCAAGTTGATTTCCAGACCATATCAAGAGACAAATGGGTCTA 1316
DB 1169 GCCTCTCAGAGCTCATCAACAGGCTTGTTCGGGACATGTTTCGACGGCAAAATGGCCCC 1228
QY 1317 AGCTTC 1322
DB 1229 AACTTC 1234

		FILE REFERENCE: BB-1171	
		CURRENT APPLICATION NUMBER: US/09/347,801	
		CURRENT FILING DATE: 1999-07-02	
		EARLIER APPLICATION NUMBER: 60/092,438	
		EARLIER FILING DATE: July 10, 1998	
		NUMBER OF SEQ ID NOS: 23	
		SOFTWARE: Microsoft Office 97	
		SEQ ID NO 9	
		LENGTH: 1814	
		TYPE: DNA	
		ORGANISM: Zea mays	
		US-09-347-801-9	
		Query Match 33.9%; Score 590; DB 3; Length 1814;	
		Best Local Similarity 72.5%; Pred. No. 2.3e-158;	
		Matches 764; Conservative 0; Mismatches 290; Indels 0; Gaps 0;	
QY	189	GTCTATCGCCATGCTGATGATAGGAGATCCCTGCTGCTGTAGTGTGATGACATGAT	248
DB	321	GGCAGTATGAGCATAAAGGACGACAAAGGAGCTTGAAGATATTGTAGTCAATGGCAATGG	380
QY	249	CAAGTCACTGGTCAATATTATCCACACATCGGTGGCAAAATCGTGAACCAAAACAG	308
DB	381	GCGAGCGCTGCTATATCATAGTACCAAGCAATGATGGAGAAATGGCAGCAAGCAG	440
QY	309	ACAAATTAGTTACATGCGGAGCGAGTTGTTGGTACAGAGCTCGTTCGGGATCGTTTTCCAA	368
DB	441	ACCAATTAGTTACATGCTGAGCGGTGTTAGTTCATGAGTCTTCCGAACCGTTTTCCAG	500
QY	369	GCAAAATGTTTGGAGACTGGAGAAACCGTGGCGATAAAGAAGTTTTCGAAGATAGAAG	428
DB	501	GCAAGTGTCTTGAACCTGTGAGACCGTAGCTATAAAAAAGGTTCTTCAAGACAAGAGA	560
QY	429	TACAAGAACCGAGAACTTCAGTTGATGCGTGTGATGGATCATCCGAATGTGGTTGTTTG	488
DB	561	TACAAGAACTGTGAGCTGCAAAACCATCGAGTGTCTTGACCAACCAATGTGGTGGCTCTA	620
QY	489	AAGCATTTGCTCTTTTCGACTACAGAGAAGACGAGCTTTTCTTGAACCTTGGTTATGGAG	548
DB	621	AAGCATTTGCTCTTCTCAAAGACTGAGAAGAGGAGCTTTTACCTCAATTTGGTGTGAG	680
QY	549	TATGTCCTCGAGACGTTGTATCGAGTTCTGAACATTATATAGTAGTGCAACCAAGAATG	608
DB	681	TATGTACCGGAGACTGCTCATCTGTGTCAACAACTTACAAAGATGAACCGCGCATG	740
QY	609	CCTCTTGTCTATGTTAAACTTTTACAGTTATCAGATCTTCGGGGACTTGTCTACATTCAC	668
DB	741	CCTTTGATTTATGCAAAACTGTATATGTATCAGATTTGTAGAGCCTTGGCATATCTCAC	800
Query Match 33.9%; Score 590; DB 4; Length 1814;			
Best Local Similarity 72.5%; Pred. No. 2.3e-158; Indels 0; Gaps 0;			
Matches 764; Conservative 0; Mismatches 290; Indels 0; Gaps 0;			
QY	189	GTCTATCGCCATGCTGATGATAGGAGATCCCTGCTGCTGTAGTGTGATGACATGAT	248
DB	321	GGCAGTATGAGCATAAAGGACGACAAAGGAGCTTGAAGATATTGTAGTCAATGGCAATGG	380
QY	249	CAAGTCACTGGTCAATATTATCCACACATCGGTGGCAAAATCGTGAACCAAAACAG	308
DB	381	GCGAGCGCTGCTATATCATAGTACCAAGCAATGATGGAGAAATGGCAGCAAGCAG	440
QY	309	ACAAATTAGTTACATGCGGAGCGAGTTGTTGGTACAGAGCTCGTTCGGGATCGTTTTCCAA	368
DB	441	ACCAATTAGTTACATGCTGAGCGGTGTTAGTTCATGAGTCTTCCGAACCGTTTTCCAG	500
QY	369	GCAAAATGTTTGGAGACTGGAGAAACCGTGGCGATAAAGAAGTTTTCGAAGATAGAAG	428
DB	501	GCAAGTGTCTTGAACCTGTGAGACCGTAGCTATAAAAAAGGTTCTTCAAGACAAGAGA	560
QY	429	TACAAGAACCGAGAACTTCAGTTGATGCGTGTGATGGATCATCCGAATGTGGTTGTTTG	488
DB	561	TACAAGAACTGTGAGCTGCAAAACCATCGAGTGTCTTGACCAACCAATGTGGTGGCTCTA	620
QY	489	AAGCATTTGCTCTTTTCGACTACAGAGAAGACGAGCTTTTCTTGAACCTTGGTTATGGAG	548
DB	621	AAGCATTTGCTCTTCTCAAAGACTGAGAAGAGGAGCTTTTACCTCAATTTGGTGTGAG	680
QY	549	TATGTCCTCGAGACGTTGTATCGAGTTCTGAACATTATATAGTAGTGCAACCAAGAATG	608
DB	681	TATGTACCGGAGACTGCTCATCTGTGTCAACAACTTACAAAGATGAACCGCGCATG	740
QY	609	CCTCTTGTCTATGTTAAACTTTTACAGTTATCAGATCTTCGGGGACTTGTCTACATTCAC	668
DB	741	CCTTTGATTTATGCAAAACTGTATATGTATCAGATTTGTAGAGCCTTGGCATATCTCAC	800
QY	669	AGTTGCGCGGAGTTTGTACAGAGATCTAAAGCCTCAAAATCTTCTGGTTGATCTCTTT	728
DB	801	ACAGCAATTGGAGTGTGCCACAGGACATTAAGCGCGCAAAATCTCTGGTTAATCTCTAT	860
QY	729	ACTCATCAAGTCAAAATCTGTGACTTTGGCAGTGGCAAAACAGCTCGTTAAAGGTGAACCA	788
DB	861	ACCATCAGCTAAAAATTGTGTGACTTTGGCAGCGCAAAAGTTCTGGTAAAAAGCGCAACCA	920
QY	789	AACATTTCTTACATCTGCTCAGATTTACAGTCTTCCGGTGCACCCGAGCTCATATTTGGTGCAC	848
DB	921	AACATTTCTTACATCTGTTCTTAGTGTACTACAGAGCTCCAGAGCTCATATTTGGTGTACT	980
QY	849	GAGTACACAACTTCTATTGATATCTGCTGCTGCTGTTGTTGTTCTTCTGCTGAGCTTCTTCTT	908
DB	981	GAATACACAAAGCATTGATTTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTA	1040
QY	909	GGTCAGCATTATTTCCTCGGAGAAATTCGTGTGATCAGCTCGTGGAAATTTATTAAGTT	968
DB	1041	GGAAGCCTCTGTTTCTCGGAGAAAGCGGTGTTGATCAGCTTGTGAAATTCATCAAGTTT	1100
QY	969	CTTGGTACACCAACTCGAGAGAAATCCGTTGTATGATCCCACTACACAGATTTTCAAG	1028
DB	1101	CTGGGCACACCCACAGTGAAGAAATTAAGTGTGATGAATCCAAATTTATACCGAGTTTAA	1160

Qy	669	AGTTGCCGGAGHTTGTGACAGAGATCTAAAGCCTCAAAATCTTCTGGTGTATCTCTT	728
Db	801	AACAGCAATTGGAGTGTGCCACAGGACATTAAGCGCAAAATCTCTGTGTTAATCTCTCAT	860
Qy	729	ACTCATCAAGTCAAAATCTGTGACCTTTGGCAGTSCGAAACAGCTCGTTAAAGGTGAACCA	788
Db	861	ACCATCAGCTAAATTTGTGTGACTTTGGCAGCGGAAAGTTCTGGTAAAGGGGAACCA	920
Qy	789	AACATTTTCTTACATCTGCTCAGCATTTCTACCGTGCACCCGAGCTCATATTTGGTGCCACT	848
Db	921	AACATTTTCTTACATCTGTTCTAGGTACTACAGAGCTCCAGAGCTCATATTTGGTGCTACT	980
Qy	849	GAGTACACAACCTTCTATTTGATACTCTGCTCTGCTGTTGTGTTCTTGCTGAGCTTCTTCTT	908
Db	981	GAATACACAACAGCCATTTGATTTGGGTCTGCTGCTGTGCTGCTGAGCTGCTTCTTA	1040
Qy	909	GGTGAGCCATTATTTCCCGGAGAAATGCTGTGGATCAGCTCGTGGAAATATTAAAGTT	968
Db	1041	GGACAGCCTCTGTTTCCCTCGAGAAAGCGGTGTGATCAGCTGTGTGAAATCATCAGGTT	1100
Qy	969	CTTGSTACACCAACTCGAGAGAATAACCGTTGTATGAATCCCACTACAGAGTTTCAAG	1028
Db	1101	CTGGGCACACCCACACGTGAAGAAATTAAGTGATGAATCCAAATATATACCGAGTTTAA	1160
Qy	1029	TTCCACAGATTAAGGCCATCTCCCTGGCACAAGATCTTCCACAAGAGATGCCCCAGAA	1088
Db	1161	TTCCCGAAATCAAAGCTCACCCATGGCATAAAGATATTCCATAAAGGATGCCGTGTGAA	1220
Qy	1089	GCGTTCATTTGGCATCAAGCTGTCTTCAATCTCTCAAGTCTTAAGATGCACAGCGCTC	1148
Db	1221	CGGTGAGATCTGTTGTCAGGCTTCTGAGTATCTACACAAATCTCGGTGCAGCTGTTTG	1280
Qy	1149	GAAGCTTTGACATCCGTTCTTTTGATGAACCTCAGAGAACCAACGCTCGTTTACCAAAT	1208
Db	1281	GAAGCATTTGTTCCATCCGTTCTTTTGATGAACCTTCGGGATCCAAACACCCGCTTACCGAAT	1340
Qy	1209	GGAGCGCTCTCCGGCTCTCTTCAACTTCAAAC	1242
Db	1341	GGTGTTTTCTTCGGCTCTCTTCAATTTTAAAG	1374

RESULT 6

Qy	614	TGTCATATGTTAAAC	TTACAGT	TATCAGAT	CTCTCCGGG	CACTTGC	TTCACAT	TTGCACAG	TTG 673
Db	629	GATATATGTGAAAC <th>CTCTATACATACAGAT</th> <th>CTTTTAGGGCG</th> <th>TTATCTTATAT</th> <th>TATTCATCG</th> <th>TTG 688</th> <td></td> <td></td>	CTCTATACATACAGAT	CTTTTAGGGCG	TTATCTTATAT	TATTCATCG	TTG 688		
Qy	674	CCGGGAGT <th>TTGTTCACAGAGAT</th> <th>CTAAAGCCTCAAAAT</th> <th>CTTCTCGTTG</th> <th>TATCTCTTACTCA</th> <th>733</th> <td></td> <td></td>	TTGTTCACAGAGAT	CTAAAGCCTCAAAAT	CTTCTCGTTG	TATCTCTTACTCA	733		
Db	689	TATTGGAGT <th>CTGCCATCGGGAT</th> <th>TCAAGCCTCAAAAT</th> <th>CTATTGGT</th> <th>CAATCCACACACTCA</th> <th>748</th> <td></td> <td></td>	CTGCCATCGGGAT	TCAAGCCTCAAAAT	CTATTGGT	CAATCCACACACTCA	748		
Qy	734	TCAAGTCAAAAT <th>CTGTGACTTTTGGCAGT</th> <th>CGCAACAGCTCGT</th> <th>TTAAAGGTGAAC</th> <th>CAACAAACAT</th> <th>793</th> <td></td> <td></td>	CTGTGACTTTTGGCAGT	CGCAACAGCTCGT	TTAAAGGTGAAC	CAACAAACAT	793		
Db	749	CCAGGTAAAT <th>TATGTGACTTTTGGAA</th> <th>GTGCAAAAGTTTGGT</th> <th>TAAAGGGCAAC</th> <th>CAAAATAT</th> <th>808</th> <td></td> <td></td>	TATGTGACTTTTGGAA	GTGCAAAAGTTTGGT	TAAAGGGCAAC	CAAAATAT	808		
Qy	794	TTCTTACAT <th>CTGCTCAGATTCTACCGT</th> <th>GCACCCGAGCTCATAT</th> <th>TTTGGTGCCA</th> <th>CTCAGTGA</th> <th>853</th> <td></td> <td></td>	CTGCTCAGATTCTACCGT	GCACCCGAGCTCATAT	TTTGGTGCCA	CTCAGTGA	853		
Db	809	ATCATACAT <th>TATGTTCTAGATACTATAGAG</th> <th>CACCTGAGCTCATAT</th> <th>TTTGGCGCAACTGA</th> <th>TA</th> <th>868</th> <td></td> <td></td>	TATGTTCTAGATACTATAGAG	CACCTGAGCTCATAT	TTTGGCGCAACTGA	TA	868		
Qy	854	CACAAC <th>TTCTATTGATATCTGGT</th> <th>CTCTGCTGTTGTGTTCT</th> <th>TGCTGAGCTTCTTCTTGGTCA</th> <th>913</th> <td></td> <td></td> <td></td>	TTCTATTGATATCTGGT	CTCTGCTGTTGTGTTCT	TGCTGAGCTTCTTCTTGGTCA	913			
Db	869	TACTACAGC <th>CAATTGACGCTCTGGTCTGTTGGAT</th> <th>GTGTTTGTAGCTGAGCTGCTGTTGGACA</th> <th>928</th> <td></td> <td></td> <td></td> <td></td>	CAATTGACGCTCTGGTCTGTTGGAT	GTGTTTGTAGCTGAGCTGCTGTTGGACA	928				
Qy	914	GCCATTAT <th>TTCCCGGAGAAAA</th> <th>TGCTGTGGATCAGCTCGCTGGAAAT</th> <th>TATTAAAGTTCTTGG</th> <th>973</th> <td></td> <td></td> <td></td>	TTCCCGGAGAAAA	TGCTGTGGATCAGCTCGCTGGAAAT	TATTAAAGTTCTTGG	973			
Db	929	GCCTCTG <th>TTCCCTGGTGAGAGTGGAGTTGATCAACT</th> <th>TTGTTGAGATCATCAAG</th> <th>TTCTTGGG</th> <th>988</th> <td></td> <td></td> <td></td>	TTCCCTGGTGAGAGTGGAGTTGATCAACT	TTGTTGAGATCATCAAG	TTCTTGGG	988			
Qy	974	TACACCAACT <th>TCGAGAGAAAA</th> <th>TCGGTTGTATGAATCCCACTACACAGAT</th> <th>TTCAAGTTCCC</th> <th>1033</th> <td></td> <td></td> <td></td>	TCGAGAGAAAA	TCGGTTGTATGAATCCCACTACACAGAT	TTCAAGTTCCC	1033			
Db	989	CAC <th>TTCCCAACAAGGAGAGATTAAGTGCATGAAC</th> <th>CCCTAATTATACAGNA</th> <th>TTTAAATCCC</th> <th>1048</th> <td></td> <td></td> <td></td>	TTCCCAACAAGGAGAGATTAAGTGCATGAAC	CCCTAATTATACAGNA	TTTAAATCCC	1048			
Qy	1034	ACAGATAA <th>AGGCCCATCCCTCGGCACAAGAT</th> <th>CTTTCCCAAAAAGATGCCCCCAGAGCGGT</th> <th>1093</th> <td></td> <td></td> <td></td> <td></td>	AGGCCCATCCCTCGGCACAAGAT	CTTTCCCAAAAAGATGCCCCCAGAGCGGT	1093				

US-09-347-801-13
Sequence 13, Application US/09347801
Patent No. 6262345
GENERAL INFORMATION:
APPLICANT: Allen, Steve
APPLICANT: Lee, Jian Ming
TITLE OF INVENTION: Plant Protein Kinases
FILE REFERENCE: BB-1171
CURRENT APPLICATION NUMBER: US/09/347,801
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: 60/092,438
EARLIER FILING DATE: July 10, 1998
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Microsoft Office 97
SEQ ID NO 13
LENGTH: 1429
TYPE: DNA
ORGANISM: Glycine max
FEATURE:
NAME/KEY: unsure
LOCATION: (1202)
FEATURE:
NAME/KEY: unsure
LOCATION: (1237)
FEATURE:
NAME/KEY: unsure
LOCATION: (1297)
FEATURE:
NAME/KEY: unsure
LOCATION: (1340)

Db 1049 ACAGATTAAAGCACATCCATCCATGCGACAAAGATCTTCCATAAGCGCATGCCCTCCAGAGGCTGT 1108
QY 1094 TGATTTGGCATCAAGGCTGCTTCAATACCTCTCAAGTCTTAAGATGACAGAGCGCTCGAAGC 1153
Db 1109 TGATTTGGTATCAAGACTACTCAATACCTCCCTAACTTGGCGGTGACAGAGTTTATAGATGC 1168
QY 1154 TTGTGCACATCCGTT---CTTTGATGAACCTCAGAGAACCAAAACGCTCGTTTACCAAATGG 1210
Db 1169 CTGGAGCGACCCCTTTCCTTTGGAGCAATTCGNGATCCAAATCCCTCGCTTGGCAANTGG 1228
QY 1211 AGGCGCTCTCCCGCCTCTCTTCAACTTCAAAACAA 1244
Db 1229 GCGATCCNTCCAACTAATTAATTCAAACCCA 1262

RESULT 7

US-09-854-731-13

; Sequence 13, Application US/09854731

; Patent No. 6794561

; GENERAL INFORMATION:

; APPLICANT: Allen, Steve

; APPLICANT: Lee, Jian Ming

; TITLE OF INVENTION: Plant Protein Kinases

; FILE REFERENCE: BB-1171

; CURRENT APPLICATION NUMBER: US/09/854,731

; CURRENT FILING DATE: 2001-05-14

; PRIOR APPLICATION NUMBER: 60/092,438

; PRIOR FILING DATE: July 10, 1998

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: Microsoft Office 97

; SEQ ID NO 13

; LENGTH: 1429

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1202)

; NAME/KEY: unsure

; LOCATION: (1237)

; NAME/KEY: unsure

; LOCATION: (1297)

; NAME/KEY: unsure

; LOCATION: (1340)

; NAME/KEY: unsure

; LOCATION: (1376)

; NAME/KEY: unsure

; LOCATION: (1410)

; NAME/KEY: unsure

; LOCATION: (1416)

US-09-854-731-13

Query Match 30.5%; Score 530.4; DB 4; Length 1429;

Best Local Similarity 69.5%; Pred. No. 2.3e-141;

Matches 733; Conservative 0; Mismatches 318; Indels 3; Gaps 1;

QY 194 TATCGCATGGCTGATGATAAGAGATCGCTGCTGTAGTTGATGGACATCATCAAGT 253
Db 209 TATGAANATTAGGATGATAGAAATGGNAGCCAGTTGTTGATGGCAACGGAACGGA 268
QY 254 CACTGGTTCATATTATTTCCACCAATCGGTGGCAAAATGGTGAACCAAAACAGACAAT 313
Db 269 GACAGGACATATCATTTGTGACTACCATTTGGGGGTAGAAATGGTTCAGCCCAAGCAGACTAT 328
QY 314 TAGTTACATGGCGGAGGAGTGTGGTACAGCTGCTTCGGGATCGTTTCCAAACAAA 373
Db 329 AAGCTACATGGCAGCGGTGTGTAGGGCATGATCATTTGGAGTTGTCTTCCAGGCTAA 388
QY 374 ATGTTTGGAGACTGGGAAACCGTGGCATAAAGAGGTTTTCGAAGATAGAGATACAA 433
Db 389 GTGCTTGGAAACCGGTGAACCTGTGGCTATCAAAAGGTTCTTCAAGACAGAGGTACAA 448
QY 434 GAACCGAGAACTTCAGTTGATCGGTGTGATGGATCATCCGAATGTGGTTTGTGAAGCA 493

Db 449 GAACCGGAGCTGCAAAACAAATCGCGCTTCTTGACCAACCAATGTGCTTTGAAGCA 508
QY 494 TTGCTTCTTTTCGACTACAGAGAAAGAGAGAGCTTTTCTTGAACCTTGGTTATGAGATGT 553
Db 509 CTGTTTCTTTTCAACACACTGAAAGAGATGAACCTATACCTTTAAATTTGGTTCTCGAATATGT 568
QY 554 CCCTGAGAGCTTGTATCGAGTTCTGAAACATTTATAGTAGTGCAAAACCAAGAAATGCTCT 613
Db 569 TCTTGAACAGTTAATCGGTGATTAACATTTACACAGTTTAAACCAAGAGTGCCTACT 628
QY 614 TGTCTATGTTAAACCTTTACAGTTATCAGATCTTCGGGGAGCTTGTCTTACATTCACAGTTG 673
Db 629 GATATATGTAACCTCTATACATACAGATCTTTAGGGCGTTATCTTATATTCATCGCTTG 688
QY 674 CCGGGAGTTTGTACAGAGATCTAAAGCCTCAAAATCTTCTGTTGTAGTCTCTTACTCA 733
Db 689 TATGAGGCTCGCCATCGGGATATCAAGCCTCAAAATCTATTTGGTCAATCCACACTCA 748
QY 734 TCAAGTCAAAATCTGTGACTTTGGCAGTGCAGAAACAGCTCGTTAAAGGTGAACCAACAT 793
Db 749 CCAGGTTAAATTTATGTGACTTTGGAAGTGCAGAGTTTGGTAAAGGCGAACCAATAT 808
QY 794 TTCTTACATCTGCTCAGATCTTACCGTGACCCGAGCTCATATTTGGTGCACCTGAGTA 853
Db 809 ATCATACATATGTTCTAGATACCTATAGAGCACCTGAGCTCATATTTGGGCGCAACTGAATA 868
QY 854 CACAACTTCTATTGATATCTGCTGCTGCTGTTGTTCTTCTGCTGAGCTTCTTCTGCTCA 913
Db 869 TACTACAGCAATGTGAGCTCTGGTCTGTTGGATGTGTTTAGCTGAGCTGCTGCTTGAGCA 928
QY 914 GGCATTTATTTCCCGGAGAAATGCTGTGATCAGCTCGTGGAAATTTATTAAGTTCTTGG 973
Db 929 GCCTCTGTTCCCTGGTGGAGTGGAGTTGATCAACTTGTGAGATCATCAAGGTTCTGGG 988
QY 974 TACACCACTCGAAGAAATCCGTTGTATGATATCCCACTACACAGATTTCAAGTTCCC 1033
Db 989 CACTCCACAGAGGAAGAGATTAAGTGCATGAACCCCTAAATATACAGAAATTTAAATTTCC 1048
QY 1034 ACAGATAAGGCCCATCCCTGGCAGCAAGATCTTCCACAAAGATGCCCCAGAACGCT 1093
Db 1049 ACAGATTAAAGCACATCCATGGCAGCAAGATCTTCCATAAGCGCATGCCCTCCAGAGGCTGT 1108
QY 1094 TGATTTGGCATCAAGGCTGCTTCAATCTCTCAAGTCTCAAGTGCACAGCGCTCGAAGC 1153
Db 1109 TGATTTGGTATCAAGACTACTACATCTCCCTTAACCTTGGGTGCACAGTTTATAGATGC 1168
QY 1154 TTGTGCACATCCGTT---CTTTGATGAACCTCAGAGAACCAACGCTGCTGTTCACAAATGG 1210
Db 1169 CTGGACGCAACCTTTCTTTGGACGAATTCGNGATCCAAATCTCTCGCTTGCCTCAATGG 1228
QY 1211 AGGCGCTCTCCCGCCTCTCTTCAACTTCAAAACAA 1244
Db 1229 GCGATCCNTCCAACTAATTAATTCAAACCCA 1262

RESULT 8

US-09-566-921-24

; Sequence 24, Application US/09566921

; Patent No. 668288

; GENERAL INFORMATION:

; APPLICANT: Loring, Jeanne F.

; APPLICANT: Tingley, Debora W.

; APPLICANT: Edwards, Carla M.

; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE

; FILE REFERENCE: PA-0024 US

; CURRENT APPLICATION NUMBER: US/09/566,921

; CURRENT FILING DATE: 2000-05-05

; NUMBER OF SEQ ID NOS: 138

; SOFTWARE: PERL Program

; SEQ ID NO 24

; LENGTH: 1952

; TYPE: DNA

; ORGANISM: Homo sapiens

FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. 6682888 234735.15
US-09-566-921-24

```

Query Match      23.0%; Score 399.6; DB 4; Length 1952;
Best Local Similarity 65.0%; Pred. No. 8e-104; Indels 6; Gaps 2;
Matches 623; Conservative 0; Mismatches 329;

QY 285 GGCAGAAATGTTGAACCAACAGACAAATAGTTACATGCGGAGCGAGTTGTTGGTACA 344
DB 212 GGCAGAGCCAGAGCGCTCCCAAGAGTGGCTTACCGGACATCAAAGTGATTGGCAAT 271
QY 345 GGCCTGTTGCGGATCGTTTTCAGCAAAATGTTTGGAGACTGGAGAACCCGTCGGGATA 404
DB 272 GGCCTCATTTGGGGTCTGTACCAGGCAACCGCTGGCAGAGACCCAGGGAACATAGTCGCCATC 331
QY 405 AAGAAAGTTTTCAGAGATAGAGATACAGAACCCAGAACTTCAGTTGATGCTGTGATG 464
DB 332 AAGAAAGTTTTCAGAGACAGAGGTTCAAGAACCCAGAGCTGCAGATCATGGTTAAGCTG 391
QY 465 GATCATCCGAATGTTGTTTGAAGCAATTCCTTTTTCGACTACAG---AGAAAGAC 521
DB 392 GACCACTGCAATATTGTGAGGCTGAGATATCTTTTCTACTCCAGTGGCGAGAGAAAGAC 451
QY 522 GAGCTTTTCTTGAACTTGGTTAAGAGTATGTCCTGAGACGTTGTATCGAGTTCTGAAA 581
DB 452 GAGCTTTTAACTAAATCTGCTGCTGAATATATGTCGCGAGACAGTGTACCGGTCGCCGCG 511
QY 582 CATTATAGTAGTGCACAAACCAAGATGCTCTTGTCTATGTTAACTTTACAGTTATCAG 641
DB 512 CACTTTCACCAAGGCCAAGTTGACCACTTCCCTATCTATGTCAGGTTGTACATGTACCAG 571
QY 642 ATCTTCCGGGACTTGTCTTACATTCACAGTTCGCCGGAGTTTGTACAGAGATCTAAAG 701
DB 572 CTCCTCCGAGCTTGGCTTACATCAC---TCCGAGGGGCTGTGTACCGGACATCAAG 628
QY 702 CCTCAAAATCTTCTGTTGATCCTCTTACTCATCAAGTCAAAATCTGTGACTTTGGCAGT 761
DB 629 CCCAGAACTCTGCTGTGACCTGACACTGCTGCTCCTCAAGCTCTGCGATTTGGCAGT 688
QY 762 GCGAAACGCTCGTTAAAGGTGAACCAACATTTCTTACATCTGCTCAGATTTACCGT 821
DB 689 GCAAGAGCTGTTGGTCCGAGGGGAGCCCAATGCTCTCTACATCTGTTCTCGTACTACCG 748
QY 822 GCACCCGAGCTCATATTTGGTGCCTGACAGTACCAACTTCTATTGATATCTGCTCTGCT 881
DB 749 GCGCCAGAGCTCATCTTTGGAGGCACTGATTAACACTCATCACTCATGATGTTTGGTCACT 808
QY 882 GGTGCTGTTCTGCTGAGCTTCTTCTGCTCAGCATTATTTCCCGGAGAAATCTGCTG 941
DB 809 GCGCTGTACTGGCAGAGCTCTCTTGGGCCAGGCCATCTTCCCTGGGAGACAGTGGGCTG 868
QY 942 GATCAGCTCGTGGAAATTTATTAAGTTCTTGGTACACCACTCAGAGAAATCGTTGT 1001
DB 869 GACCAAGCTGGTGGAGATCATCAAGTGTGCGGAACCAACCCGGGAACAAATCCGAGAG 928
QY 1002 ATGAATCCCAACTACACAGATTTCAAGTTTCCACAGATAAAGGCCCATCCCTGGCACAAG 1061
DB 929 ATGAACCCCAACTACACAGGATTTCAAGTTTCCCTCAGATTAAAGCTCACCCCTGGHCAAAG 988
QY 1062 ATCTTCCCAAAAGGATGCCCCAGAGCGGTTGATTGGCATCAAGGCTGCTTCAATAC 1121
DB 989 GTGTTCAAATCTCGAAACGCCGCCAGAGGCCATCGCGCTCTGCTCTAGCCTGCTGGAGTAC 1048
QY 1122 TCTCAAGTCTTAAGATGACAGCGCTCGAGCTTGTGACATTCGCTTCTTTGATGAATCT 1181
DB 1049 ACCCCATCTCAAGGCTCTCCCACTAGAGGCTGTGGGCAACAGCTTCTTTGATGAATCT 1108
QY 1182 AGAGAACCAACCGCTGTTTACCAATGAGCGGCTCTCCCGGCTCTCTCAACTTCA 1239
DB 1109 CGATGCTGGGAAACCCAGCTGCTTAACCAACCCGCCACATTCCTCCCTCTCTTCAACTTCA 1166

```

RESULT 9
US-09-488-856A-3
; Sequence 3, Application US/09488856A
; Patent No. 6316259
; GENERAL INFORMATION:
; APPLICANT: Robert P. Monia
; APPLICANT: Robert McKay
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXP
; FILE REFERENCE: RTS-0115
; CURRENT APPLICATION NUMBER: US/09/488,856A
; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 2154
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (92)...(1543)
US-09-488-856A-3

```

Query Match      23.0%; Score 399.6; DB 3; Length 2154;
Best Local Similarity 65.0%; Pred. No. 8.4e-104; Indels 6; Gaps 2;
Matches 623; Conservative 0; Mismatches 329;

QY 285 GGCAGAAATGTTGAACCAACAGACAAATAGTTACATGCGGAGCGAGTTGTTGGTACA 344
DB 413 GGCAGAGCCAGAGCGCTCCCAAGAGTGGCTTACCGGACATCAAAGTGATTGGCAAT 472
QY 345 GGCCTGTTTGGGATCGTTTTCAGCAAAATGTTTGGAGACTGGAGAACCCGTCGGGATA 404
DB 473 GGCCTATTGGGGTCTGTACCAGCAGCGCTGGCAGAGACCCAGGAACTAGTCGCCATC 532
QY 405 AAGAAAGTTTTCAGAGATAGAGATACAGAACCCAGAACTTCAGTTGATGCTGTGATG 464
DB 533 AAGAAAGTTTTCAGAGACAGAGGTTCAAGAACCCAGAGCTGCAGATCATGCTAAGCTG 592
QY 465 GATCATCCGAATGTTGTTTGAAGCAATTCCTTTTTCGACTACAG---AGAAAGAC 521
DB 593 GACCACTGCAATATTGTGAGGCTGAGATACCTTTTCTACTCCAGTGGCGAGAGAAAGAC 652
QY 522 GAGCTTTTCTTGAACCTTGGTATGAGTATGCTCCTGAGAGCTTGTATCGAGTTCTGAAA 581
DB 653 GAGCTTTTACCTAAATCTGCTGCTGGAATATGTCGCCGAGACAGTGTACCGGTCGCCG 712
QY 582 CATTATAGTAGTGCACAAACCAAGAGTGCCTCTTGTCTATGTTAACTTTACAGTTATCAG 641
DB 713 CACTTCAACAAAGGCCAAGTTGACCATCCCTATCTCTATGTCAAGGTGTACATGTACCAG 772
QY 642 ATCTTCCGGGACTTGTCTTACATTCACAGTTCGCCGGAGTTTGTACAGAGATCTAAAG 701
DB 773 CTCCTCCGAGCTTGGCTTACATCCAC---TCCAGGGGCTGTGTACCGGACATCAAG 829
QY 702 CCTCAAAATCTTCTGTTGATCTCTTACTCATCAAGTCAAAATCTGTGACTTTTGGCAGT 761
DB 830 CCCAGAACTTGTGTTGGACCTGACACTGCTGCTCCTCAAGCTCTGCGATTTTGGCAGT 889
QY 762 GCGAAACAGCTCGTTTAAAGGTGAACCAAACTTTCTTACATCTGCTCAAGTTTACCGT 821
DB 890 GCAAGCAGTTGGTCCGAGGGGAGCCCAATGCTCTCTACATCTGTTCTCGCTACTACCGG 949
QY 822 GCACCCGAGCTCATATTTGGTGGCCACTGAGTACACAACTTCTATTGATATCTGGTCTGCT 881
DB 950 GCGCCAGAGCTCATCTTTTGGAGCCCATGATTACCTCATCCATCGATTTTGGTCACT 1009
QY 882 GGTGTTGTTCTTGTGAGCTTCTTCTTGGTCAAGCAATTTATCCCGGAGAGAAATGCTGTG 941
DB 1010 GCGTGTGTACTGGCAGAGCTCTCTTGGGCCAGGCCATCTTCCCTGGGAGCAGTGGGCTG 1069
QY 942 GATCAGCTCGTGGAAATTTATTAAGTTCTTGGTACACCAACTCGAGAGAAATTCGTTGT 1001

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Db 1070 GACCAGCTGGTGGAGATCATCAAGTGTGGGAACCAACCGGGAACAAATCCGAGAG 1129
QY 1002 ATGAATCCCAACTACACAGATTTCAAGTTCCCAACAGATAAAGCCCATCCCTGGCACAAG 1061
Db 1130 ATGAACCCCAACTACACAGGAGTTCAAGTTCCCTCAGATTAAGCTCACCCCTGGACAAAG 1189
QY 1062 ATCTTCCAAAAAGGATGCCCCAGAAAGCGTTTGATTGGCATCAAGGCTGCTTCAATAC 1121
Db 1190 GTGTTCAATCTGAACGCCCGCAGAGGCCATCGCGCTCTAGCTCTGGAGTAC 1249
QY 1122 TCTCCAGTCTAAGATGCACAGCGCTCGAAGCTTGTGCACATCCGTTCTTTGATGAATC 1181
Db 1250 ACCCATCTCAAGGCTCTCCCACTAGAGCGCTGTGGCAGCAGCTTCTTTGATGAATG 1309
QY 1182 AGAGAACCAACCGCTGTTTACCAATAGGAGCGCTCTCCGCGCTCTCTTCAACTTCA 1239
Db 1310 CGATGTCTGGGAACCCAGCTGCCTTAACAACCGGCCACTTCCCGCTCTCTTCAACTTCA 1367

RESULT 10
US-08-602-264A-1
; Sequence 1, Application US/08602264A
; Patent No. 5837853
; GENERAL INFORMATION:
; APPLICANT: Akihiko TAKASHIMA et al.
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROFF, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,264A
; FILING DATE: February 20, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2088 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to genomic RNA
; ORIGINAL SOURCE:
; ORGANISM: human being
US-08-602-264A-1

Query Match 22.6%; Score 393.2; DB 2; Length 2088;
Best Local Similarity 63.3%; Pred. No. 5.7e-102;
Matches 637; Conservative 0; Mismatches 363; Indels 6; Gaps 2;
QY 305 ACACACAATTAGTTACATGCGGAGCGAGTGTGTGGTACAGGCTCGTTTCGGGATCGTTTT 364

RESULT 11
US-08-461-018A-1
; Sequence 1, Application US/08461018A
; Patent No. 6071694
; GENERAL INFORMATION:

Db 768 ACAAGAAGTCAGCTATACAGACACTAAACTCATTTGGAAATGGATCATTTTGGTGTGCTATA 827
QY 365 CCAAGCAAAATGTTGGAGACTGGAGAAACCGTGGCGGATAAAGAGAGTTTTCGAAGATAG 424
Db 828 TCAAGCCAAACTTTGTGATTCAGGGAACCTGGTCCGCATCAAGAAAGTATTCGAGACAA 887
QY 425 AAGATACAAGAACCCGAGAACTTTCAGTTGATGGTGTGATGGATCATCCCAATGTGTTGTG 484
Db 888 GAGATTTAAGATTCAGAGCTCCAGATCATGAGAAGCTTAGATCATCTGTAAACATAGTCCG 947
QY 485 TTTGAAGCATTTGCTCTTTTTCGACTACAG---AGAAAGACGAGCTTTTCTTGAACCTTGGT 541
Db 948 ATTGGCTTATTCTTCTACTCCAGTGGTGAAGAAAGATGAGGTCTATCTTAACTCTGGT 1007
QY 542 TATGGAGTATGCCCTCGAGACGTTGTATCGAGTTCTGAAACATATATAGTAGTGCACAAACCA 601
Db 1008 GCTGGACTATGTTCGCGAAACAGTATACAGAGTTGCCAGACATATAGTCGAGCCAAACA 1067
QY 602 AAGAATGCTCTTGTCTATGTTAAACTTTACAGTTATACAGATCTTCCGGGAGCTTCTCTTA 661
Db 1068 GAGCTCCCTCTGTGATTTATGTCAGTTGTATGTATGATCAGCTGTTCCGAAGTTTACGCTTA 1127
QY 662 CATTCACAGTTGCCCGGAGATTGTGCACAGAGATCTAAAGCCCTCAAAATCTTCTGTTGA 721
Db 1128 TATCCA---TTCCTTTTGGAAATCTGCCATCGGATATTAACCGCAGAACTCTTGTGGA 1184
QY 722 TCTCTTACTCATCAAGTCAAAATCTGTGACTTTGTGAGTTCGAGTGCAGAAACAGCTGTTAAAGG 781
Db 1185 TCTGATACTGCTGTATTAATAAACTCTGTGACTTTTGGAAAGTGCAGAGCAGCTGTCGAGG 1244
QY 782 TGAACCAAACTTTTACATCTGCTCAGATTCTACCGTGCACCGAGCTCATATTTGG 841
Db 1245 AGAACCAATGTTTGTATATCTGTTCTCGTACTATAGGACACAGAGTTGATCTTTGG 1304
QY 842 TGCCTAGTATACAACTTCTATTGATATCTGCTGCTGCTGTTGTTCTTGTCTGAGCT 901
Db 1305 AGCCACTGATTATACCTCTAGTATAGATGTATGTTCTGCTGGCTGTGTGTGCTGAGCT 1364
QY 902 TCTTCTTGTGTCAGCATTTATTCGCGGAGAAATGCTGTGGATCAGCTGTCGAAATAT 961
Db 1365 GTTACTAGGACAAACCAATATTTCCAGGGGATAGTGTGTGGATCAGTTGTGTAGAAATAAT 1424
QY 962 TAAAGTTCTTGGTACACCAACTCGAGAAGAAATCCGTTGTATGAATCCCAACTACACAGA 1021
Db 1425 CAAGGTCTTGGGAATCTCAACCAAGGAGGCAATCAGAGAAATGAAACCAACTACACAGA 1484
QY 1022 TTTCAAGTTCCACAGATAAAGCCCATCCCTGGCACAAGATCTTCCACAAAAGGATGCC 1081
Db 1485 ATTTAAATTCCTCAAAATTAAGGCACATCTTGGACTAAGGTCTTCGACCCCGAACTCC 1544
QY 1082 CCGAAGCGGTTGATTTGGCATCAAGGCTGCTTCAATACTCTCCAAGTCTAAGATGCAC 1141
Db 1545 ACCGAGGCAATTTGCACTGTGTAGCCGCTGTGGAGTATACACCAACTGCCCGACTAAC 1604
QY 1142 AGCGCTCGAAGCTTGTGCACATCCGTTCTTTGATGAACCTCAGAGAACCAACCGCTCGTTT 1201
Db 1605 ACCACTGGAAGCTTGTGCACATTTCTTTGATGATTTACGGGACCAAAATGTCAAACT 1664
QY 1202 ACCAAATGGAACGGCTCTCCCGCTCTCTTCAACTTCAAAACAAAGAGTAGTGCATCATC 1261
Db 1665 ACCAAATGGCGGAGACACACCTGCACTCTTCAACTTCCACACTCAAGAACTGTCAAGTAA 1724
QY 1262 ACCTGAACCTGGTCAACAAGTTGATTCAGACGATATCAAGAGACAA 1307
Db 1725 TCCACCTCTGGCTACCATCCTTATTCTCTCTCATGCTCGGATTCNA 1770

```

; APPLICANT: AKIHiko TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROOTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,018A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2088 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; ORIGINAL SOURCE:
; ORGANISM: human being
; US-08-461-018A-1

Query Match 22.6%; Score 393.2; DB 3; Length 2088;
Best Local Similarity 63.3%; Pred. No. 5,7e-102;
Matches 637; Conservative 0; Mismatches 363; Indels 6; Gaps 2;

QY 305 ACAGACAATTACTATGATCGGCGAGTGTGTGTACAGGCTGTTGGGATCGTTT 364
DB 768 ACAGAGTCACTATACAGACACTAACTATTGGAATGGATCATTTGGTGTGATA 827
QY 365 CCAAGCAAAATGTTGGAGACTGGAGAACCCGTGGCGATAAAGAGGTTTTCGAAGATAG 424
DB 828 TCAAGCCAACTTTGTGATTACAGAGAACTGTCGCCATCAAGAAAGTATTGCAGACAA 887
QY 425 AAGATACAGAACCGAGAACTTCAGTTGATGCGGTGTGATGATATCGGAATGTTGGTTG 484
DB 888 GAGATTAAAGATCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAACATAGTCCG 947
QY 485 TTTGAGCAATCTCTTTTTCGACTACAG---AGAAGACGAGCTTTTCTGAACTTGT 541
DB 948 ATTGGCTTATTTCTTCTACTCCAGTGGTGAAGAAAGATGAGGCTATCTTAAATCTGT 1007
QY 542 TATGAGTATGTCCTCGAGACGTTGTATCGAGTTCGAAACATATAGTAGTGCAAAACA 601
DB 1008 GCTGGACTATGTCGGAACAGATATACAGAGTTCGAGACACTATAGTCGAGCCAAACA 1067
QY 602 AAGATGCTCTGTCTATGTTAACTTTACAGTATACAGATCTTCGGGGAGCTTGTCTTA 661
DB 1068 GACGCTCCCTGTGATTTATGTCAAGTTGTATATGATATGATCAGCTGTTCCGAAAGTTAGCCTA 1127
QY 662 CATTACAGTTCCTCGGGAGTTTGTACAGAGATCTTAAGCTCAAAATCTTCTGTGTA 721
DB 1128 TATCCA---TTCCTTTGGAATCTGCCATCGGAGATATTAACCCGAGAACCTCTTGTGTA 1184

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RESULT 12
US-09-216-958-1
; Sequence 1, Application US/09216958
; Patent No. 6248559
; GENERAL INFORMATION:
; APPLICANT: AKIHiko TAKASHIMA et al.
; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROOTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/216,958
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/461,018
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367

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QY 722 TCCTCTTACTCATCAAGTCAAAATCTGTGACTTTTGGCAGTGGCAACAGCTCGTTAAAGG 781
DB 1185 TCCTGATACTGCTGTATTAAAACTCTGTGACTTTTGGAAAGTGCAGAGCAGCTGTCGAGG 1244
QY 782 TGAACCAACAATTTCTTACATCTGCTCAGATTTCTACCGTGCACCGAGCTCATATTTGG 841
DB 1245 AGAACCCAAATGTTTCTGTATATCTGTTCTCGGTACTATAGGGCAGCAGAGTTGATCTTTGG 1304
QY 842 TGCCACTGAGTACACAACTTTCTATTGATATCTGTGCTGCTGCTGTTGTTCTTGTGAGCT 901
DB 1305 AGCCACTGATTATACCTCTAGTATAGATGATGTTGTTGCTGCTGCTGTTGCTGAGCT 1364
QY 902 TCTTCTTGGTACGCCATTTATTTCCCGGAGAAATGCTGTGAGTACAGCTCGTGGAAATTTAT 961
DB 1365 GTTACTAGGACAAACCAATATTTCCAGGGGATAGTGTGTGGATCAGTTTGGTGAATAAT 1424
QY 962 TAAAGTTCTTGTGTACACCAACTCCGAGAGAAATCGTTGTATGAAATCCCAACTACACAGA 1021
DB 1425 CAAGTCTCTGGAACTCCCAACAGGGAGCAAAATAGAGAAATGAACCCAACTACACAGA 1484
QY 1022 TTTCAAGTTCCACAGATAAAGGCCCATCCCTGGCACAAGATCTTCCACAAAAGGATGCC 1081
DB 1485 ATTTAAATTCCTCAATTAAGGCACATCTCTTGGACTTCTTCCGACCCGAACTCC 1544
QY 1082 CCCAGAACGGTTGATTTGGCATCAAGCTGCTTCAATATCTCTCAAGTCTTAAGATGCAAC 1141
DB 1545 ACCGAGGCAATTTGCACTGTGTAGCCGTCTGTGGAGTATACACCAACTGCCCGACTAAC 1604
QY 1142 AGCGTCTGAAGCTTGTGCACATCCGTTCTTTGATGAACTCAGAGAACCAAGAGCTCGTTT 1201
DB 1605 ACCACTGGAAGCTTGTGCACATTTCAATTTTGTGAAATTTACGGGACCCCAATGTCAAAC 1664
QY 1202 ACCAAATGGAGCGGCTCTCCGCGCTCTCTTCAACTTTCAAAAGAGTAGCTGGATCATC 1261
DB 1665 ACCAAATGGCGAGACACACTGCACTCTTCAACTTCCACTCAGAACTGTCAAGTAA 1724
QY 1262 ACCTGAACTGTGTCAAAGTGTGATTTCCAGACATATCAAGAGACAA 1307
DB 1725 TCCACCTCTGGCTACCCTTATTTCTCTCTCATCTCGGATTCAA 1770

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; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2088 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; ORIGINAL SOURCE:
; ORGANISM: human being
; US-09-216-958-1

Query Match      22.6%; Score 393.2; DB 3; Length 2088;
Best Local Similarity 63.3%; Pred. No. 5.7e-102;
Matches 637; Conservative 0; Mismatches 363; Indels 6; Gaps 2;

QY 305 ACAGACAATTTAGTTACATGCGGCGAGCTGTTGGTACAGGCTCGTTGGGATCGTTTT 364
DB 768 AAGAAGTCAGCTATACAGACTAACTCATTTGGAATGGATCATTTGGTGTGTATA 827
QY 365 CCAAGCAAAATGTTTGAGACTCGAAGAACCGTGGCGATAAAGAGGTTTTGCAAGATAG 424
DB 828 TCAGGCCAACTTTGTGATTCAGAGAACTGTCGCCATCAAGAAAGTATTCAGAGCAA 887
QY 425 AAGATCAAGAACCGAGAACTTCAGTTGATGCGTGTGATGATCATCCGAAATGTTGTTG 484
DB 888 GAGATTAAAGATCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAACATAGTCGG 947
QY 485 TTTGAGCATGCTCTTTTCGACTACAG---AGAAAGCAGCTTTCTTGAACTTGGT 541
DB 948 ATTGCGTATTTCTTCTACTCCAGTGGTGAAGAAAGATGAGGTCTATCTTAATCTGGT 1007
QY 542 TATGGAGTATGTCCTCGAGACGTTGATCGAGTTCTGAAACATTTAGTAGTCAAAACCA 601
DB 1008 GCTGGACTATGTCGGAACACAGTATACAGAGTTGCGACACATATAGTCGAGCCAAACA 1067
QY 602 AAGAAATGCTTGTCTATGTTAAACTTTACAGTTATCAGATCTTCGGGGAGCTTCCTTA 661
DB 1068 GACGCTCCCTGTGATTTATGTCAAAGTTGATATGATCAGCTGTTCCGAAAGTTTAGCCTA 1127
QY 662 CATTACAGTTGCGGGAGTTGTCACAGAGATCTAAGACCTCAAAATCTCTGTTGA 721
DB 1128 TATCCA---TTCTTTTGGAACTGCGCATCGGGATATTAACCCGAGAACCTCTGTGTGA 1184
QY 722 TCCTCTTACTCATCAAGTCAAAATCTGTGACTTTTGGCAGTGCAGAAACAGCTCGTTAAAGG 781
DB 1185 TCCTGATACGTGTTAANAATCTGTGACTTTTGGAAAGTGCAGACGCTGGTCCGAGG 1244
QY 782 TGAACCAAAATTTTACATCTGTCTCAAGATCTACCGTGCAACCGAGCTCATATTGG 841
DB 1245 AGAACCCAAATGTTTCGTATATCTGTTCTCGTACTATAGGSCACAGAGTTGATCTTTGG 1304
QY 842 TGCACCTGAGTACACAACCTCTATTGATATCTGCTGCTGGTGTGTTCTTCCTGAGCT 901
DB 1305 AGCCACTGATATACCTCTAGTATAGATGATGGTCTGCTGGCTGTGTTGCTGAGCT 1364
QY 902 TCTTCTTGGTCAGCAATTTATCCCGGAGAAATATGCTGGAATCAGCTCGTGGAAATAT 961
DB 1365 GTTACTAGGACACCAATATTTCCAGGGGATAGTGTGTGGATCAGTTGTTAGAAATAT 1424
QY 962 TAAAGTTCTTGGTACACCAATCTCGAGAGAAATCCGTTGATGAATCCCAACTACACAGA 1021
DB 1425 CAAGGCTCTGGAACTCCAAAGAGGAGCAAAATCAGAGAAATGAAACCCAAACTACACAGA 1484
QY 1022 TTTCAAGTCCCAAGATTAAGGCCATCCCTGGCACAGATCTTCCACAAAAGGATGCC 1081
DB 1485 ATTAAATTCCTCAAAATTAAGGCACATCTTGGACTAAGGTCTTCGACCCCGAACTCC 1544
QY 1082 CCCAGAACCGGTTGATTTGGCATCAAGGCTGCTTCAATCTCTCCAAGTCTAAGATGCAC 1141
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RESULT 13
US-09-489-765A-3
; Sequence 3, Application US/09489765A
; Patent No. 6323029
; GENERAL INFORMATION:
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRESSION
; FILE REFERENCE: RTS-0124
; CURRENT APPLICATION NUMBER: US/09/489, 765A
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 85
; SEQ ID NO 3
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (40)...(1302)
US-09-489-765A-3
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Query Match      22.5%; Score 391.6; DB 3; Length 1389;
Best Local Similarity 63.2%; Pred. No. 1.3e-101;
Matches 636; Conservative 0; Mismatches 364; Indels 6; Gaps 2;
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QY 305 ACAGACAATTTAGTTACATGCGGCGAGCTGTTGGTACAGGCTCGTTGGGATCGTTTT 364
DB 192 ACAGAGTCAGCTATACAGACACTAAAGTATTGAAATGGATCATTTGGTGTGTATA 251
QY 365 CCAAGCAAAATGTTTGAGACTGGAGAACCGTGGCGATAAAGAGGTTTGCAGATAG 424
DB 252 TCAAGCCAAACTTTGTGATTCAGAGAACTGGTCCGCATCAAGAAAGTATTGCAGGACA 311
QY 425 AAGATACAGAACCGAGAACTTCAGTTGATGCTGTGATGATCATCCGAATGTTGTTG 484
DB 312 GAGATTAAAGATCGAGAGCTCCAGATCATGAGAAAGTAGATCATCTGAACATAGTCCG 371
QY 485 TTTGAGCATGCTCTCTTTTCGACTACAG---AGAAAGCAGCTTTCTTGAACCTTGGT 541
DB 372 ATTGCGTATTTCTTCTACTCCAGTGTGAGAGAAAGATGAGTCTATCTTAATCTGGT 431
QY 542 TATGGAGTATGTCCTCGAGACGTTGATCGAGTTCTTGAAACATATATAGTAGTCAACCA 601
DB 432 GCTGGACTATGTTCCGAAACAGTATACAGAGTTGCCAGACACTATAGTCGAGCCAAACA 491
QY 602 AAGATGCTCTTGTCTATGTTAACTTTACAGTTATCAGATCTTCGGGGACTTCCTTA 661
DB 492 GACGCTCCCTGTGATTTATGTCAAAGTTGATATGATAGTCTGCTTCGAAAGTTAGCCTA 551
QY 662 CATTACAGTTGCGGGAGTGTGTCAAGAGATCTAAGAGCTCAAAATCTTCTGTTGA 721
DB 552 TATCCA---TTCTTTTGGATCTGCCATCGGATATTAAACCGAGAACTCTTGTGGA 608
QY 722 TCCTCTTACTCATCAAGTCAAAATCTGTGACTTTGGCAGTTCGGAACAGCTCGTTAAAGG 781
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Query Match 82.4%; Score 1431.6; DB 21; Length 1490;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1460; Conservative 0; Mismatches 29; Indels 1;

QY 921 TTCCCGGAGAAAATGCTGTGGATCAGCTCGTGGAAATTTATTAAGTCTTGTGTACACCA 980
 DB 721 TTTCGCGGAGAAAATGCTGTGGATCAGCTCGTGGAAATTTATTAAGTCTTGTGTACACCA 780
 QY 981 ACTCGAGAAAGAAATCCGTTGTATGAATCCCAACTACACAGATTTCAAGTTCCACAGATA 1040
 DB 781 ACTCGAGAAAGAAATCCGTTGTATGAATCCCAACTACACAGATTTCAAGTTCCACAGATA 840
 QY 1041 AAGGCCATCCCTGGGACAGAGATCTTCCACAAAGGATGCCCCAGAGCGGTTGATTGG 1100
 DB 841 AAGGCACATCCCTGGGACAGAGATCTTCCACAAAGGATGCCCCAGAGCGGTTGATTGG 900
 QY 1101 GCATCAAGGCTGCTTCAATACTCTCAAGTCTAAGATGACACGCGCTCGAAGCTTGTGCA 1160
 DB 901 GCATCAAGGCTGCTTCAATACTCTCAAGTCTAAGATGACACGCGCTCGAAGCTTGTGCA 960
 QY 1161 CATCCGTTCTTTGATGAATCATGAGAAACCAAGCGCTCGTTTACCAATGGAGCGGCTCTTC 1220
 DB 961 CATCCGTTCTTTGATGAATCATGAGAAACCAAGCGCTCGTTTACCAATGGAGCGGCTCTTC 1020
 QY 1221 CGGCTCTCTTCAACTTCAAAAGAGTAGCTGGATCATCACTGAACTGGTCAACAG 1280
 DB 1021 CGGCTCTCTTCAACTTCAAAAGAGTAGCTGGATCATCACTGAACTGGTCAACAG 1080
 QY 1281 TTGATTCAGACCATATCAAGACAAATGGGCTAAGCTTCTTGAATCAATCTGGAAT 1340
 DB 1081 TTGATTCAGACCATATCAAGACAAATGGGCTAAGCTTCTTGAATCAATCTGGAAT 1140
 QY 1341 TAA 1343
 DB 1141 TAA 1143

RESULT 4

US-10-292-408-15
 ; Sequence 15, Application US/10292408
 ; Publication No. US20030182692A1
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN THIELEN, NOCHA
 ; APPLICANT: DA COSTA E SILVA, OSWALDO
 ; APPLICANT: CHEN, RUOYING
 ; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METHODS
 ; TITLE OF INVENTION: OF USE IN PLANTS
 ; FILE REFERENCE: 16313-0178
 ; CURRENT APPLICATION NUMBER: US/10/292,408
 ; PRIOR FILING DATE: 2002-11-12
 ; PRIOR FILING DATE: 60/346,096
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 15
 ; LENGTH: 1621
 ; TYPE: DNA
 ; ORGANISM: Brassica napus
 US-10-292-408-15

Query Match 60.9%; Score 1058.4; DB 16; Length 1621;
 Best Local Similarity 81.5%; Pred. No. 8.9e-295;
 Matches 1307; Conservative 0; Mismatches 271; Indels 26; Gaps 6;
 QY 75 TCCCTTTCTCTCTATCGGCCACATGATCATGACCAACCAAACTGATTGAAACTCATTT 134
 DB 8 TCTCTCTCTCTCTCCACATTTGATGATCATTTACCAACCAAACTAATTGAAATCCATTT 67
 QY 135 GTCTCTCTCTCTCAAAATCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 194
 DB 68 GTTCTCTCTCTCTC--TCTCTCTCTCTCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 125
 QY 195 ATGCCCATGGCTGATGATAGGAGAT---GCCCTGCTGCTGCTAGTGTGATGGACATGATCAA 251
 DB 126 AAGCTATGGCTGACGATAGGAGATGCCCGCGGCTGCTGTAGTGTGATGGACATGACCAA 185
 QY 252 GTCACTGGTCATATTATTTCCACCACAAATCGTGGCAAAATGGTGAACCAAAACAGACA 311

DB 186 GTCACTGGCCACATAATCTCCACCACCTCGGTGTTAAAAACGAGAAACCAAAAACAGACA 245
 QY 312 ATTAGTTACATCGCGGAGCGAGTTGTTGGTACAGGCTCGTTCCGGATCGTTTCCAGCA 371
 DB 246 ATAAAGTTACATCGCGGAGCGAGTTGTCGGTACAGGCTCCTTCGGGATAGTGTTCAGGGC 305
 QY 372 AAATGTTGGAGACTGGAGAAACCGTGGCGATAAAGAGGTTTTCGCAAGATAGAATAC 431
 DB 306 AAGTGTCTGGAGACTGGAGAAACCGTGGCGATAAAGAGGTTTTCGCAAGAGGATAC 365
 QY 432 AAGAACCGAGAACTTTCAGTTGATGCGTGTGATGAGATCATCCGAATGTGTTGTTGAAG 491
 DB 366 AAGAACCGAGAGCTTTCAGCTGATGCGTGTGATGGAACCAATCCGAAATGTTGTTGAAG 425
 QY 492 CATTCGCTCTTTCGACTACAGAGAAAGACGAGCTTTCCTGAACTTGGTGTAGGATAT 551
 DB 426 CATTCGCTCTTTCGACCAAGAGACGAGCTTTCCTGAACTTGGTGTAGGATAT 485
 QY 552 GTCCCTGAGACGTTGTATCGAGTTCTGAAACATTAAGTAGTGCAAAACCAAGAAATGCCT 611
 DB 486 GTCCCTGAGAGCTTGTACCGAGTTCTGAAACATTAAGTAGTGCAAAACCAAGAGATGCCG 545
 QY 612 CTGTCTATGTTAAACTTTTACAGATTATCAGATCTTTCGGGAGCTTGTTCATTCACAT 671
 DB 546 CTGTGTTATGTTAAACTCTATATGATACAGATCTTTCAGAGGACTTGTTCATTCACAT 605
 QY 672 TCCCGGGAGTTTGTACAGAGATCTTAAGCCTCAAAATCTTCTGGTGTAGTCTCTTACT 731
 DB 606 GTTGTGGAGTTTGTACAGAGATCTTAAGCCTCAAAATCTTCTGGTGTAGTCTCTTACT 665
 QY 732 CATCAAGTCAAAATCTGTGACTTTGGCAGTGGCAAAACAGCTCGTTAAAGGTGAACCAAAAC 791
 DB 666 CATCAAGTCAAGATCTGTGATTTGGCAGTGGCAAAACAGCTTGTAAAGGTGAAGCCAAC 725
 QY 792 ATTTCTTACATCTGCTCAGATTTACCGTCAACCGAGCTCATATTTGGTGCACATGAG 851
 DB 726 ATCTCTTACATATGTTCAAGATTTACCGTCAACCGTCAACCTGAATTTATTTCCGTGCACTGAG 785
 QY 852 TACACAACTTCTATTGATATCTGCTCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 911
 DB 786 TACACAACTTCTCAATTGATATTTGGTCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 845
 QY 912 CAGCCATTTATCCCGGAGAAAATGCTGTGGATCAGCTCGTGGAAATTTATTAAGTTCCT 971
 DB 846 CAGCCATTTATCCCGGAGAAAATGCTGTGGTCTGCTGTTGTTGTTGTTGTTGTTGTTGTT 905
 QY 972 GTTACACCAACTCGAGAGAAATCCGTTGTATGAATCCCAACTACACAGATTTCAAGTTC 1031
 DB 906 GTTACACCAACTCGAGAGAGATCCGTTGTATGAATCCCAACTACACAGATTTTAGGTTTC 965
 QY 1032 CCACAGATAAAGGCCATCCCTGGCACAAGATCTTCCACAAAGGATGCCCCAGAGCG 1091
 DB 966 CCGCAGATAAAGGCACATCTTGGCACAAGATTTTCCACAAAGGATGCCCTCCAGAGCC 1025
 QY 1092 GTTGTATTTGGCATCAAGGCTGCTTCAATCTCTCAAAGTCTAAGATGCAAGGCTCGAA 1151
 DB 1026 ATTTGATTTGGCATCAAGGCTGCTTCAAGTCTCTCAAGTCTTAGATGCAAGGCTTGAA 1085
 QY 1152 GCTTGTGACATCCGTTCTTTGATGAATCTCAGAGAAACCAAGCGCTCGTTTACAAATGGA 1211
 DB 1086 GCTTGTGACATCCGTTCTTTGATGAGCTTAGAGAACCAAAATGCTCGTTTACCAACCGGA 1145
 QY 1212 CGGCTCTCTCCGCTCTCTTCAACTTCAACAGAGTAGTGGATCATCACTGCACTGAACTG 1271
 DB 1146 CGGCTCTCTCCGCTCTCTTCAACTTCAACAGAGTAGTGGAGCTTCACTGAGCTG 1205
 QY 1272 GTCAACAAAGTTGATTCAGACCATATCAAGAGCAATTTGGGCTAAGCTTCTTGAATCAA 1331
 DB 1206 GTCAACAAAGTTGATTCAGACCATATCAAGAGCGAGTTGGTCTAAGCTTCTTGAATCAG 1265
 QY 1332 TCTGGAACTTAAAGGGATCTCGCAAAAGACAACTACTTTTATATATATAA--TGTACCAT 1390

Db 1266 TCTGGAACCT-AAACAAAGCATCAAAAAGACAAGAACTTTTTATATATATATGACCAT 1324
Qy 1391 TACACGAGCCCAAGGTCGTAGTTGAAGGCAAAAGCTGGAGGACACAAATTCAAAGTTTTTC 1450
Db 1325 TACTCAGAACCAAGAGAGGTTAGTTGAAGGCAAGCTGGAGGACACAGTTAGAGGTTTTGC 1384
Qy 1451 CTCCTCAAA-----CTCGTTGAGACAAAGCCAGCTGCTAGCAAAACCAAC 1495
Db 1385 CTCCTCAAACTCGTTCCAGGAATGAAGGTCAAAAAGACAAGCTTCTCTACAACTGAC 1444
Qy 1496 TACCCCAATCTGCGAAAAACAACTCTCCAGTGTGTATCTGCTT---ATTCTCTTC 1551
Db 1445 TTCCCCCAAGCTGCAAGAAAGCTACTCAGTTGTATCTTCTCTCTCTCTCTCTCTCTCT 1504
Qy 1552 TCTTTTCAAGTTGGTGAAGAAACACAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1611
Db 1505 TTTTAAAAATGTTGGTTAAAGCAAGAAACAAATCTCTCTCTCTCTCTCTCTCTCTCTCT 1564
Qy 1612 CTTATGTAATGAGTTAGTCAGAGTTTATATATAGTAA 1655
Db 1565 GCATCTGTAATGAGTTAGTCAGAGATTTTATATAGTAA 1608

RESULT 5
US-10-425-114-12807
; Sequence 12807, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21153313 B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 12807
; LENGTH: 1726
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701212714_FLI
US-10-425-114-12807

Query Match 44.2%; Score 768.6; DB 18; Length 1726;
Best Local Similarity 77.0%; Pred. No. 6.5e-211;
Matches 936; Conservative 0; Mismatches 279; Indels 0; Gaps 0;

Qy 129 TCATTGTCTCTCTCTCTCAATCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 188
Db 20 TCTTTCTCTCTCTCTCTCGACCATTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 79
Qy 189 GTCTCTATCGGCATGGCTGATGAAGAGATGCTGCTGCTGTAGTTGATGGACATGAT 248
Db 80 CTCCTCTCGGCATGGCTGAGATGAAGAGATGCTGCTGCTGATCAATGGGATGAT 139
Qy 249 CAAGTCATGGTCAATATTTTCCACCAATCGGTGGCAAAATGGTGAACCAAAACAG 308
Db 140 TCCCTAACTGGTCAATATCTACAACTATTGGAGGCAAAATGGGAAACCCCAACAG 199
Qy 309 ACAATTAGTACATCGCGGAGGAGTTGTTGTCAGAGCTGTTCTGGGATGTTTTC 368
Db 200 ACTATTAGTACATCGCGAGAACGGTTGTAGGAATGATCAATTTGGAATCGTTTTCAG 259
Qy 369 GCAAAATGTTGGAGATGGAGAAACCGTGGCGATAAAGAGGTTTTCAGATAGAAGA 428
Db 260 GCAAAATGTTGGAACTGGGGAGGAGTGGCAATTAAGAGTTTTCAGAGACAGAAGA 319
Qy 429 TACAAGAACCGAGAACTTTCAGTTGATGCTGTGATGGATCATCCGAATGTGGTTGTTG 488

Db 320 TACAAGAACTGTAACCTGCAAGTTAATGCGTGTGATGATCATCCAAATGTGATCTCTTG 379
Qy 489 AAGCAATGCTCTCTTTTCGACTACAGAGAAAGACGAGCTTTTCTTGAATCTGTTATGAG 548
Db 380 AAGCAATGCTCTTTTCAACTACAGTACAGATGAATCTTTTCAATTTGGTGATGAG 439
Qy 549 TATGTCCTGAGAGCTGTTGATGAGTTCGAAACATATATAGTGTGCAAAACCAAGAAATG 608
Db 440 TATGTTCCAGAGTCCATGTATAGAGTCTTAAAGCACTATAGCAATGCTAAATCAAGAAATG 499
Qy 609 CCTCTGTCTATGTTTAAACTTTACAGATATCAGATCTTCCGGGAGCTTGTCTTACATTCAC 668
Db 500 CCAATCATCTACGTAAGAACTTTATATGACAGATTTTCAAGGGGTTGGCTTTACATCCAC 559
Qy 669 AGTTGCCCGGAGTTTGTCCAGAGATCTAAAGCCTCAAAATCTTCTGTTGATCTCTCT 728
Db 560 ACTGTCCTCAAGTTTGGCCACAGAGATTTGAAGCCTCAAAATATATATCTGTTGATCTCT 619
Qy 729 ACTCATCAAGTCAAAATCTGTGACTTTGGCAGTGGAAACAGCTCGTTAAAGGTGAACCA 788
Db 620 ACACACCAAGTGAAGCTATGTGATTTTGAAGTGCAAAAGTTCTAGTCAAGGTGAAGCT 679
Qy 789 AACATTTCTTACATCTGCTCAGGATTTCTACCGTGCACCCGAGCTCATATTTTGGTGCCT 848
Db 680 AATATATCATACATATGTTTCAGATTTCTATCGAGCACCAGAACTTATATTTGGGGCCACA 739
Qy 849 GAGTACACAACTTCTTATGATATCTGCTGCTGCTGTTGTTCTTCTGCTGAGCTTCTCTCT 908
Db 740 GAGTATACCACTTCTGATGATATTTGTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 799
Qy 909 GGTGAGCCATTTATCCCGGAGAAATGCTGTGATCAGCTGCTGGAATATTTAAAGTT 968
Db 800 GGCCAGCCATTTATCCCTGGCGAAATGCACTAGACCAGCTTGTACATATTTATAAAGGTG 859
Qy 969 CTTGCTACACCACTCGAGAGAAATCCGTTGTATGATGATCCCACTACACAGATTTCAAG 1028
Db 860 CTTGGCACACCCACCGAGAGGAAGTACGCTGTATGAAATCCCAATTTACAATGACTTTAGG 919
Qy 1029 TTCCACAGATAAAGGCCATCCCTCGCACAAGATCTTCCACAAAGGATGCCCCAGAA 1088
Db 920 TTTCCACAGATAAAGCACACCCATGGCACAAGATTTTCCACAAAGAGATGCTCCAGAA 979
Qy 1089 CGGTTGATTTGGCATCAAGCTGCTTCAATCTCTCAAGTCTAAGATGCAACAGGCTC 1148
Db 980 GCTATTGATCTTGCATCCCGCTTTTGCATCTCTCCCAAGTCTCCGGTGCACCTGCTT 1039
Qy 1149 GAAGCTTGTGCATCCGTTCTTTGATGAACTCTCAGAGAACCAAGCTGCTTACCAAT 1208
Db 1040 GAAGCATGTGCATCTCTTTCTTTGATGAACTTCTGTAACCTTAATGCTGCTGCTGCTGCT 1099
Qy 1209 GGAGGCTCTCCGCTCTCTTCAACTTCAAAAGAGTAGCTGGAATCATCACTGAA 1268
Db 1100 GGTGTCATTTCCCTCTCTTAACTTCAACAGGAATTTATCTGGAGCATCTTCCGAG 1159
Qy 1269 CTGGTCAACAGTTGATTTCCAGACCATATCAAGAGCAATTTGGGTTAAGCTTCTGAA 1328
Db 1160 CTTGTTAATAGTTGATACCTGACCATGTGAAGGGCAATGGGGATACAGTTTATGCT 1219
Qy 1329 CAATCTGGAACCTTAA 1343
Db 1220 CTGGGAGGATCGTGA 1234

RESULT 6
US-10-424-599-67990
; Sequence 67990, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei


```
QY 409 AGGTTTTCAGATAGACATACAGAACCGAGAACTTCAGTTGATGCTGTGATGGATC 468
Db 342 AGGTTTTCAGACAGACAGATACAGAAATCGTGAATACAGTTAAATGCGTGTGATGGATC 401
QY 469 ATCCGAATGTGGTTTGTGTTGAAGACATGCTCTTTTCGACTACAGAGAAAGACGAGCTTT 528
Db 402 ATCCAAATGTGATCTCTTTGAAGCATGTTCTTTTCCACTACAGTACTGATGAATTT 461
QY 529 TCTTGAACCTTGTTATGGAAGTATGTCCTTCGAGACGTTGTTGATCGAGTTCTGAAACATTTATA 588
Db 462 TTCTTAAATTTGGTGTAGATATGTTCCAGAGTCCATGATATAGAGTCTTTAAAGCACTACA 521
QY 589 GTAGTGCAACCAAGAAATGCTCTTGTCTATGTTTAACTTTTACAGTTATCAGATCTTCC 648
Db 522 GCAATGCTAATCAAGAAATGCTCTATCATCTAGTTTAACTTTTATATGTACCAAGATTTTCA 581
QY 649 GGGGAGCTTCTTACATTTACAGTTGCGCGGAGTTTGTCCAGAGATCTTAAAGCTCTCAA 708
Db 582 GGGGGTGGCTTATATCCACATGTTTCCCAAAGTTTGCACAGAGATTTGAAGCTCTCAA 641
QY 709 ATCTTCTGTTGATCTCTTATCTATCAATCAAGTCAAAATCTGTGACTTTGGCAGTGCAGAAC 768
Db 642 ATATCTGTTGATCTCTTACACCAAGTGAAGCTATGTGACTTTTGAAGTGCAGAAC 701
QY 769 AGCTGTTAAAGTGAACCAACATTTCTTACATCTGCTCAGCATTTCTACGTCACCGG 828
Db 702 TTCTAGTCAAGGTGAAGCTAATATATCATATATATTTTACGGTTCTATCGAGCACCAG 761
QY 829 AGCTCATATTTGGTGCACAGTACACAACTTCTATGATATCTGTTGCTGCTGTGTTG 888
Db 762 AACTCATATTTGGGCGCACAGATATACAAATCTCAATGATATTTGTTGAGTGTGCTGTG 821
QY 889 TTCTTCTGAGCTTCTTCTTGTGTCAGCCATTTTCCCGGAGAAAATGCTGTGATCAGC 948
Db 822 TCCTTGTGAACTTCTTTTGGCGCAGCAATTTATCCCTGCGCAAAATGCAAGTAGACCAGC 881
QY 949 TCGTGAATTAATTAAGTTCTTGTGTACACCACTTCGAGAGAAATCGGTTGTATGAATC 1008
Db 882 TTGTACATATTAAGGTGCTTGGCAGCCCACTCGAGAGGAAGTACGCTGTATGAATC 941
QY 1009 CCAACTACACAGATTTCAAGTTTCCACAGATAAAGCCCATCCCTGGCACAAGATCTTCC 1068
Db 942 CCAATTTACATGACTTTAGTGTTCCTCAGATTAAGACACACCNTGGCAAGATATTTCC 1001
QY 1069 ACAAAGGATGCCCCAGAGCGGTGTGATTTGGCATCAAGGCTGCTTCAATACTCTCCAA 1128
Db 1002 ACAAAGAGTCTCGGAAGCTATGTATCTTGGATCCCGGCTGTTGCAATACTCCCAA 1061
QY 1129 GTCTAAGATGCAAGCGCTCGAAGCTTGTGCAATCCTCGTTCTTTGATGAATCTCAGAGAAC 1188
Db 1062 GTCTCGGTGCACTGCACTTGAAGCATGTGCAATCTCTTCTTTGATGAATCTCGTGAAC 1121
QY 1189 CAAACGCTGTTTACCAATGACGCGCTCTCCGCTCTCTTCACTTCAACCAAGAG 1248
Db 1122 CCAACGCTGCGCTGCCAAATGTCGCGCAATTTCCCGCTCTTATTAATCTTCAACAGGAAT 1181
QY 1249 TAGCTGGATCATCAGCTGAACTGGTCAACAAGTTGATTCAGACCATATCAAGAGACAAAT 1308
Db 1182 TATCTGGAGCATCTCCGAGCTTGTATTAAGTTGATTAATCTGACCATGTCAGGAGCGGCAA 1241
QY 1309 TGGGTCTAAGCTTCTTGAATCAATCTGGAATTTAA 1343
Db 1242 TGGGGCTACAATTTATGATCTCTGGGAGGATCGTGA 1276
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RESULT 8

US-10-764-138-6

; Sequence 6, Application US/10764138

; Publication No. US20050081266A1

; GENERAL INFORMATION:

; APPLICANT: Sudwestdeutsche Saatzeucht-SWS

; APPLICANT: Advanta Seeds B.V.

; TITLE OF INVENTION: Modulation of Storage Organs

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; FILE REFERENCE: 026-1
; CURRENT APPLICATION NUMBER: US/10/764,138
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/09/578,194
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1636
; TYPE: DNA
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)..(1636)
; OTHER INFORMATION: strain Columbia ecotype
; OTHER INFORMATION: taxon:3702
; OTHER INFORMATION: tissue type leaves
; OTHER INFORMATION: clone lib lambda ZAPII development stage young shoots
; PUBLICATION INFORMATION:
; AUTHORS: Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lecharny, A. and Kreis, M.
; TITLE: Three New cDNAs Related to SGG/GSK-3 ( Shaggy/Glycogen Synthase Kinase-3)
; TITLE: from Arabidopsis thaliana ( Accession No. X94938, x94939 and X99696) ( PGR97-
; TITLE: 008)
; JOURNAL: Plant Physiol.
; VOLUME: 113
; ISSUE: 1
; PAGES: 306-306
; DATE: 1997-01-01
; DATABASE ACCESSION NUMBER: genbank/X94938
; DATABASE ENTRY DATE: 1998-02-13
; RELEVANT RESIDUES: (1)..(1636)
US-10-764-138-6
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Query Match 42.3%; Score 734.6; DB 21; Length 1636;
Best Local Similarity 77.5%; Pred. No. 4.3e-201;
Matches 890; Conservative 0; Mismatches 259; Indels 0; Gaps 0;

QY 197 CGCATGCTGATGATGATAGGAGATGCTGCTGCTGTAGTTGATGACATGATCAAGTGCAC 256
Db 137 CGATATAGACAAACACAGAGGAATGCTGCTGCTGTTATAGAGGAATGATGCTGTTAC 196
QY 257 TGGTCATATTTTCCACCAATCGGTGGCAAAATCGTGAACCCAAACACACAAATTAG 316
Db 197 CGGTACATATTTTCTACTCAATTTGGAGGCAAAATGTTGAACCTAAACAGACCATTAG 256
QY 317 TTACATGCGGAGCGAGTTGTTGTACAGGCTCGTTTCCGGATCGTTTCCAGCAAAATG 376
Db 257 TTACATGCGGAGCGAGTTGTTGTGGAACAGGATCATTCGGAATTTGTTCCAGGCAAAATG 316
QY 377 TTTGAGACTGCGAGAAACCGTGGCGATAAAGAGGTTTTCAGAGATAGAGATACAAGAA 436
Db 317 CTTGAAACTCGAGAACTCAGTAGCCATTAAGAGGTTTTCAGAGATCGCGTTATAAAAA 376
QY 437 CGGAGAACTTCAGTTGATGCTGTGATGATCATCCGATGCTGTTGTTGAAAGCATTG 496
Db 377 CCGAGAGTTGCAATTAATGCGACTTAATGACCATCAAAATGTTGTTTCTTGAAGCATTG 436
QY 497 CTCTTTTTCGACTACAGAGAAAGACGAGCTTTTCTTGAACCTTGGTTATGGAGTATGTCC 556
Db 437 TTTCTTCTTACACGACTAGAGATGAGCTCTTCTCTCATCTCGTTATGGAGTATGTACC 496
QY 557 TGAGACGTTGTATCGAGTTCTGAAACATTAATAGTAGTGCAAAACCAAGAAATGCCTCTGT 616
Db 497 AGAGACATTTGACCGGGTTTGAAGCACTATATACTAGTTCAAACCAAGCGGATGCTATCT 556
QY 617 CTATGTTAACTTTTACAGTTATCAGATCTTCGGGGACTTCGTTACATTCACAGTTGCC 676
Db 557 CTATGTTCAAACTTTTACACATACCAAACTTCAGAGGCTTGGCTTATATATCTACTGCTCC 616
QY 677 GGGAGTTTGTACAGAGATCTAAAGCCCTCAAAATCTCTCTGGTTGATCTCTTACTCATCA 736
Db 617 TGGTGTCTGCCACAGAGATATAAACCAAAATCTTTTGGTTGATCTCCACACCCATCA 676
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FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_83691C.1
US-10-424-599-124786

Query Match 39.8%; Score 688.2; DB 18; Length 2519;
Best Local Similarity 76.5%; Pred. No. 1.5e-187;
Matches 882; Conservative 0; Mismatches 268; Indels 3; Gaps 3;

QY 197 CGCCATGGCTGATGATAAGGAGATGCTGCTGCTGATGTTGATGGACATGAT-CAAGTCA 255
DB 783 CGATATGGAGACCGATGAAGATATGTCAGTCTCTGTCATTTAGGGGAATGATGACGTTA 942

QY 256 CTGGTCAATATATTTCCACCACAATCGGTGGCAGAAATGTTGAACCAAAACAGACAATTA 315
DB 843 CTGGCCACATAATCTCCACCACAATTTGGAGGCAAAATGGGAACTTAACAGACCATCA 902

QY 316 GTTACATGGCGGAGCGAGTTGTTGGTACAGGCTCGTTTCGGGATCGTTTTCAGAGCAAAAT 375
DB 903 GTTACATGGCAGAACGTTGTTGGCACTGGATCATTTGGAGTGTGTTTCCAGGCAAGT 962

QY 376 GTTTGGAGACTG-GAGAAACCGTGGCGATAAAGAGGTTTTCGAAGATAGAGATACAG 434
DB 963 GCTTGAGACTGGGAGGCGAGTGGCTATTAAGAGGCTTTGCAAGACAGGCGATACAA 1022

QY 435 AACCGAGAACTTCAGTTGATGCGTGTGATGATCATCCGAATGCGTTGTTTGAAGCAT 494
DB 1023 AATCGAGAAATTCAGTTAATGCGCTTAATGGATCACCCAAATCTAATACATGAAGCAC 1082

QY 495 TGTCTCTTTTCGACTACAGAGAAAGA-CGAGCTTTTTCGAACTTGGTATGGATGATGT 553
DB 1083 TTTTAAATTTCTCATCAAGCAAGATCCAACTTTTCTAAACTTGTATGAGATATGT 1142

QY 554 CCTGAGAGCGTTGATCGAGTCTGAAACATATAGTAGTGCAAAACCAAGATGCTCT 613
DB 1143 CCTGAGTCAATCAACCGAATTAATCAACATACACTACTATTAAACAGAGATGCTCT 1202

QY 614 TGTCTATGTTAAACTTTACAGTTATCAGATCTTCGGGGACTTGTACATTCACAGTTG 673
DB 1203 CATCTACGTGAATCTGTATACATATCAATCTTCAGGGATTAGCATATATCCATCCGC 1262

QY 674 CCGGAGATTTGTCACAGAGATCTAAGCTCTAAATCTTCTGGTTGATCTCTTACTCA 733
DB 1263 CCTGCGAGTTTGGCATAGGATGTAAGCTCTAAATCTTTTGGTTTCATCTCTTACTCA 1322

QY 734 TCAAGTCAAAATCTGTGACTTTTGGCAGTGGCAACAGCTGTTTAAAGGTGAACCAACAT 793
DB 1323 CCAAGTTAAGCTAATGTTTGGGAGTGCAGAAAGTTCTGGTCAAGGGTGAATCAAACT 1382

QY 794 TTCTTACATCTGCTCAGATTTACCGTGCACCGAGCTCATATTTGGTGCCACTGAGTA 853
DB 1383 TTCTACATATGTTCAAGTTACTATCGGGCTCCAGAACTAATATTTGGTGCACTGAATA 1442

QY 854 CACAATCTTATTTGATATCTGGTCTGCTGTTGTTCTTGGTTGATCTCTTCTGGTCA 913
DB 1443 CACACCTTCTATTTGATATCTGGTCAAGTGTGTTCTTCTGCTGAACCTCTCTAGGACA 1502

QY 914 GCCATTATTTCCCGGAGAAATCTGTGGATCAGCTCGTGGAAATTAATAAGTTCTTGG 973
DB 1503 GCCATTGTTTCTGGAGAAATCAGGTGGACCAACTTGTGGAAATTAATAAGTTCTTGG 1562

QY 974 TACACAACTCCGAGAGAAATCCGTTGTATGAATCCCACTACACAGATTTCAAGTTCCC 1033
DB 1563 TACTCCGACTCGAGGAATCCGTTGATGAACCCAAATTAACAGATTTAGATTTCC 1622

QY 1034 ACAGATAAAGGCCCATCTCTGGCAAGATCTTTCACAAAGAGATGCCCCCAAGCGGT 1093
DB 1623 TCAGATTAAGAGCTCATCTTGGCACAAGGTTTTCACAAGCGAATGCTCTCAAGCAAT 1682

QY 1094 TGAATGGCATCAAGGCTGCTCAATCTCTCAAGTCTTAAGATGCACAGCGCTCGAGC 1153
DB 1683 TGACCTTGATCAAGGCTTCTCAATATTCACCTAGTCTACGCTGCACGCTCGTGAAGC 1742

QY 1154 TTGTGCACATCCGTTCTTTGATGAATCTCAGAGAACCAACGCTCGTTTACCAATGGACG 1213

DB 1743 ATGTGCACATCTTTCTTTGATGAGCTTCGCGAGCAAAATGCGCTCTCTCTAAATGGCCA 1802

QY 1214 GCCTCTCCGCTCTCTTCAACTTCAACAAAGAGTGTGATCATCACCTGAACTGGT 1273

DB 1803 TCCACTGGCCCCACTTTTCAACTTCAACAGAGTGTAGCTGGAGCATCACCTGAACTGAT 1862

QY 1274 CAACAAAGTTGATTCAGAGCCATATCAAGAGACAAATTTGGTCTTAAGCTTCTTGAATCAATC 1333

DB 1863 CAATAGGCTCATCCAGAGCATATTAAGCGGAGATGGTCTCAGCTTCCCGCATCTCTGC 1922

QY 1334 TCGAACTTAAAG 1346

DB 1923 CGGTTCATAGATG 1935

RESULT 12
US-10-437-963-29872/c
; Sequence 29872, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 29872
; LENGTH: 1922
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_34331C.1
US-10-437-963-29872

Query Match 39.4%; Score 685.4; DB 19; Length 1922;
Best Local Similarity 75.5%; Pred. No. 8.2e-187;
Matches 851; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

QY 224 TGTCTGCTGATGATGGACATGATCAAGTCACTGTCTATATTATTTTCCACCAATTCGG 283

DB 1703 TGTCTCTTATGGAAGGAGTGTCTGTCTCACCGGCCACATAATCTCCACACGATTGG 1644

QY 284 TGGCAAAATGCTGACCAAAACAGACAAATTTAGTTACATGGCGGAGCGAGTTGTTGGTAC 343

DB 1643 AGGGAAGATGGAGAACCTTAAAGGACGATTAGTACATGGCAGAACGAGTTGTGGGAAC 1584

QY 344 AGGCTCGTTCCGGATCGTTTTTCAAGCAAAATGTTTGGAGACTGGAGAAACCGTGGCGAT 403

DB 1583 TGGATCATTTGGAATCGTCTTTCAGCAAAATGTTTGGAGACTGGTGGAGACTGTCCGCAT 1524

QY 404 AAAGAAGGTTTTTCCAGATAGAGATAAAGAACCGAGAACTTTCAGTTGATGCTGTGAT 463

DB 1523 TAAGAAGGTTTTTACAGGACAGCGTTTACAAAGAACAGGAGTTGCGAGATTATGCGATCAAT 1464

QY 464 GGATCATCCGAATGGTTTGTGTTGAGCATTTCTTTTTCGACTACAGAGAAAGACGA 523

DB 1463 GGATCATTCGAATGTTGTTTCTTTTGAAGCATTTGCTTCTTCTACAAACAGAGAGATGA 1404

QY 524 GCTTTTCTTGAATCTGGTTATGAGTATGTCCTGAGAGCTGTATTCGAGTTCTGAAACA 583

DB 1403 ACTTTTCTTAACTGCTGATGGAATTTGTTCTCTGAGTCACTGATCTGTGTTGAAGCA 1344

QY 584 TTATAGTAGTGCAAACCAAGAAATGCTCTTGTCTATGTTAAACTTTTACAGTTATCAGAT 643

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Db 1343 TTATAGACATGAACCAAGGATGCCACTATATATGTCAATTTGATGTTTACCAGAT 1284
Qy 644 CTTCCGGGAGCTTGCTTACATTCACAGTTGGCCGGGAGTTTGTCTCAGAGATCTAAAGCC 703
Db 1283 ATTCCGTGGTTGGCTTACATTCATACCTGACCTGAGTTTCCACAGGATGTGAAGCC 1224
Qy 704 TCAAAATCTTCGTGGTTGATCTTACTCATCAAGTCAAAATCTGTGACTTTGGCAGTGC 763
Db 1223 TCAGAACTCTTTGGTGGATCTTACTCACCAGTCAAAATATGTGATTTTGGGAGGCG 1164
Qy 764 GAAACAGCTCGTTAAAGGTGAACCAAAATTTCTTACATCTGCTCACGATTTCTACCGTGC 823
Db 1163 AAAAAATGTTGTTAAAGGTGAACCAACATATCGTATATATGTTCAAGTTATACCGTGC 1104
Qy 824 ACCGAGCTCATATTTGGTGGCCAGTACAACTCTTATGATATCTGTCTGTGTCG 883
Db 1103 TCCAGAACTGATATTTGGGCGCAACCGAATACACGACATCAATGATATATGTCAGCTGC 1044
Qy 884 TTGTTGTTCTGCTGAGCTTCTTCTGTTGTCAGCATATTTCCCGGAGAAATGCTGTGA 943
Db 1043 GTGTGTTCTGCTGAGTTGCTCTTGGCCAGGCTCTCTTCTGTTGTAAGTGCAGTGA 984
Qy 944 TCAGCTCGTGGAAATTAATAAGTTCTTGGTACACCAACTCGAGAAAGAAATCCGTTGTAT 1003
Db 983 TCAGCTTGTGAGATTAATAAGTTCTTGGTACTCCACACGCTGAGAAATCCGTTGCAT 924
Qy 1004 GAATCCCAACTACAGATTTCAAGTTCCCAAGATAAAGGCCCATCCCTGGCAACAAGAT 1063
Db 923 GAATCCCAACTACAGATTTCAAGTTCCCAAGATAAAGGCCCATCCCTGGCAACAAGAT 864
Qy 1064 CTTCCACAAAGGATGCCCCGAGAGCGGTTGATTTGGCATCAAGGCTGCTTCAATACTC 1123
Db 863 TTTCACAAAGCGGATGCCCCGAGAGCGGTTGATTTGGCATCAAGGCTGCTTCAATACTC 804
Qy 1124 TCCAAAGTCTAAGATGACACAGCGCTGCAAGCTTGTGACATCCGTTCTTTGATGAATCA 1183
Db 803 ACCAAATCTACATGACAGCTGCTCGAAGCATGTGACATTCATTTCTTTGATGAATTCG 744
Qy 1184 AGAACCAACGCTCGTTTACCAAAATGGACGGCTCTCCGCGCTCTCTTCAACTTCAAAACA 1243
Db 743 AGAACCCCAAGCAAGGTTGCCAAATGGACGTCATTTCCCGCCACCTGTTCAACTTAAAGCA 684
Qy 1244 AGAAGTAGCTGATCATCACTGAACTGTCAAGTTGATTTCCAGACCATATCAAGAG 1303
Db 683 AGAAGTAGCTGATCATCACTGAACTGTCAAGTTGATTTCCAGAGGTTGATACCAGAGCATGCTCGGCG 624
Qy 1304 ACAATTGGGCTTAAGCTCTTCAATCAATCTGCACTTAAAGGGAT 1350
Db 623 ACATTGGGTTCAATTTCTTGCTGCTCCCGACCATAGGAGCGCT 577

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RESULT 13

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US-10-425-115-22950/c
; Sequence 22950, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(5322)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 22950
; LENGTH: 1779
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRF4577_120933C.1
US-10-425-115-22950

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Query Match 39.0%; Score 678.4; DB 20; Length 1779;
Best Local Similarity 75.4%; Pred. No. 8.3e-185;
Matches 844; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

Qy 223 CTGCTGCTGTAGTTGATCGACATGATCAAGTCACTGGTCAATATTTTCCACCAACAATCG 282
Db 1529 CTGCTGCTGTATGATGAGGGAATGATCCAGTCACGGGTCAATATATCTCAACAACATG 1470
Qy 283 GTGGCAAAATTTGGTGAACCAAAACAGACAAATTTAGTTATACATGCGGAGGAGTTGTGTA 342
Db 1469 GAGGGAAGAATGGAGAGCTTAAAGAGCTATCAGCTACATGCGACAGAGAGTTGTGGGA 1410
Qy 343 CAGGCTCGTTGGGATCGTTTCCAGCAAAATGTTTGGAGACTGCGAGAAACCGTGGCGA 402
Db 1409 CTGGATCATTCGGAAATCGTCTTCAGGCAAAATGTTTGGAGACTGCGTGGAGACTGTTGCTA 1350
Qy 403 TAAAGAAGGTTTTCAGACATAGACATACAAAGACCGAGAACTTCCAGTTGATGCGTGA 462
Db 1349 TCAAGAGGTTTTCAGGACAGCGCTACAAAGACAGGAGCTGCAAAATCATGCGATCCA 1290
Qy 463 TGGATCATCCGAATGTTGTTTGAAGCAATGCTTCTTTTCGACTACAGAGAAAGAG 522
Db 1289 TGGATCACTGCAATGCTGTTTCTTGAAGCAATGTTTCTTCTCCACCAACAGCAGATG 1230
Qy 523 AGCTTTCTTGAACTTGGTTATGAGATATGTCCTCGAGAGCTTGTATCGAGTTCTGAAAC 582
Db 1229 AACTTTTCTTAACTTAGTGTGAGTTGTTCTCTGAGTCACTACATCGTGTCTGAAGC 1170
Qy 583 ATTAGTAGTGAACCAAAAGAAATGCTTCTTCTATGTTTAAACTTTACAGTTATACAGA 642
Db 1169 ACTACAGCAATATGAACAGAGAGTGGCGCTTATTTATGTTAAATATATATACCTACCAGA 1110
Qy 643 TCTTCGGGAGCTTGTCTTACATTTACAGTTGCGCGGAGTTTGTACAGAGATCTAAAGC 702
Db 1109 TATTTCGAGGTTAGCTTATTTACACAGTACCTGTTGTTGCCACAGGATGTGAAC 1050
Qy 703 CTCAAAATCTTCTGTTGATCTTCTTACTCATCAAGTCAAAATCTGTGACTTTGGCAGTG 762
Db 1049 CACAGATCTTTTGGTTGATGCTTCACTCAAGTGAAGATATGTTGTTTGGGAGTG 990
Qy 763 CGAACAGCTGTTAAAGTGAACCAAAATTTCTTACATCTGCTCAGATTTCTACCGTG 822
Db 989 CAAAATGTTGTTCAAGGTGAAGCAAAATTTCTATATATATGCTCAGCTTATACCGTG 930
Qy 823 CACCGAGCTCATATTTGCTGCCACTGAGTACACAACTTCTTATGATATCTGTTCTGCTG 882
Db 929 CTCAGAGCTCATATTTGGGCAACCGAGTACACAACTCAATGATATTTGTTGCTGCTG 870
Qy 883 GTTGTGTTCTGCTGAGCTTCTTCTGTTGCTGAGCTTATTTCCCGGAGAAATGCTGTG 942
Db 869 GATGTGTTCTGCTGAGCTGCTTCTTGGCCAGGCTCTCTTCCCTGGCGAAGTGTGCTG 810
Qy 943 ATCAGCTGCTGGAATTAATAAGTTCTTGGTACACCAACTCGAGAGAAATCCCTGTA 1002
Db 809 ATCAACTGTTGAGATAATAAGGTTCTTGGTACTCCAAACAGTGAAGAAATCCCGTTGA 750
Qy 1003 TGAATCCCAACTACACAGATTTCAAGTTCCCAAGATAAAGGCCCATCCCTGGCAACA 1062
Db 749 TGAATCCCAACTACACAGGTTTAGATTTCTCAGTCAAGCTCACCCATGGCACAGA 690
Qy 1063 TCTTCCCAAAAGGATGCCCGCAGAGCGGTTGATTTGGCATCAAGGCTGCTTCAATACT 1122
Db 689 TTTTCCCAAGCGGATGCTCCAGAGCTATAGATCTCGCTTCAAGTTTGTCTCCAGTACT 630
Qy 1123 CTCAGAGTCTAAGATGACAGGCTCGAGCTTGTGCACTCCGTTCTTGTGATGACTCA 1182
Db 629 CACCAATCTAAGATGCACTGCTTCTTGAAGGCTGTGCACTCCATCTTCTTGTGATGCTG 570
Qy 1183 GAGAACCAAAAGCTGTTTACCAAAATGAGCGGCTCTCCCGCTCTCTTCAACTTCAAAAC 1242
Db 569 GAGAGCCACATGCGCGGTTGCCAAATGAGCGGCCATTTCTTCCACTGTTTCAACTTAAAC 510

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Search completed: June 24, 2005, 08:33:16
Job time : 1875.84 secs

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QY 270 TCCACCACAATCGGTGGCAAAATGCTGAACCAACCAACAGACAATTAGTTACATGCGGAG 329
Db 233 TCACACACATTTGCAGGCCAAATGCGAACCTTAACCAAAACCATCAGTTTACATGCGCGAA 292
QY 330 CGAGTTGTTGGTACAGGCTCGTTCCGGATCGTTTTCCAGCAAAATGTTTGGAGACTGGA 389
Db 293 CGTGTGTTGGCACTGGATCAATTTGGCATTTTCCAGGCGAAGTCTTGGAGACTGGC 352
QY 390 GAAACGGTGGCGATAAAGAGGTTTTCAGATAGAGATACAGAAACGAGAACTTCAG 449
Db 353 GAGGCGAGTGGCTATAAAGAAGGCTTTCAGGACAGGCGATACAAAATCGTGAACCTGAG 412
QY 450 TTGATGCGTGCATCGATCCGATCGTGTGTTTGAAGCATTTGCTTTTCGACT 509
Db 413 TTAATGCGGCTGATGATCACCAGATTAATATTTCTTGAGTAACTATTTCTTCTACA 472
QY 510 ACAGAGAAGACGAGCTTTTCTTGAACCTTGGTTATGGAGTATGTCCTCGAGACGTTGTAT 569
Db 473 ACAAGTAGAGATGAACCTTTTCTGAACCTTGGTATGGAATATGTCCTGAGACGATCTTC 532
QY 570 CGAGTTCTGAACATATAGTAGTGAACCAACCAAGAAATGCTCTTGTCTATGTTAACTT 629
Db 533 CGTGTATAAAGCACTACAGTAGCATGAACACAGAGAAATGCCCTAATCTATGTGAATTA 592
QY 630 TACAGTTATCAGATCTTCGGGGACTTGTCTTACATTCACAGTTGCCGGGAGTTGTAC 689
Db 593 TATACATATCAAACTTTTAGGGGACTGGCGTATATCCATCTGTACCAAGGAATCTGCCAT 652
QY 690 AGAGATCTAAAGCCTCAAAATCTTCTGGTTGATCTCTTACTCATCAAGTCAAAATCTGT 749
Db 653 AGGGATTTGAAGCCTCAAAATCTTTTGGTTGATCGACTCACACACCAAGTCAAGCTCTGT 712
QY 750 GACTTTGGCAGTGCAGAACAGCTCGTTAAAGGTGAACCAAAACATTTCTTACATCTGCTCA 809
Db 713 GATTTTGGCAGTGCAGAAAGTCTCGTGGAGGGTGAATCAAAACATTTCTACATATGTTCA 772
QY 810 CGATTTACCGTGCACCGGCTCATATTTGGTGCCACTGAGTACACAACTTCTATTGAT 869
Db 773 CGGTACTATCGTGCCCGCAGAGCTAATATTTGGTGGGCGAGAAATCACAACTTCTGTTGAT 832
QY 870 ATCTGCTGCTGGTGTGTTCTTCTGCTGAGCTTCTTCTTGGTCAGCCATTAATTCGCCGGA 929
Db 833 ATTTGGTCCGCTGGTTGTGCTTTGGGNACTTCTTCTAGGCCAGCCTTTGTTCCAGGA 892
QY 930 GAAATGCTGTGGATCAGCTCGTGAATTTATTAAGTTCTTGGTACACCAACTCGAGAA 989
Db 893 GAAATCAGGTTGACCAACTCGTGAATTTATCAAGATTTCTTGGCACTCCTACTCGAGAA 952
QY 990 GAAATCGGTTGATGAATCCCAACTACACAGATTTCAAGTTCCACAGATAAGGCCCAT 1049
Db 953 GAAATTCGATGATGAATCCCTAATTTATACAGATTTTCAAGTTCCCCCATATCAAGCTCAT 1012
QY 1050 CCTGGCACAAGATCTTCCACAAAAGGATGCCCCAGAGCGGTTGATTTGGCATCAAGG 1109
Db 1013 CCTTGGCATAGGTTTTCACAGCAATGCTCTCTGAAGCAATTTGACCTTGCAATCAAGG 1072
QY 1110 CTGCTTCAATCTCTCCAAGTCTAAGATGCACAGGCTCGAAGCTTGTGCAATCCGTTTC 1169
Db 1073 CTTCCTCAATATTTCCCAAACTTCGTTACAGTGCAGTGGAGCAATGGCAATCCTTTC 1132
QY 1170 TTTGATGAACCTCAGAGAACCAACGCTGTTTACCAATGGAGCGGCTCTCCCGCTCTC 1229
Db 1133 TTTGACGAGCTTCGGGAGCCCAATCCCGGCTACCTAATGGTGTGTCCTGCTCCACTT 1192
QY 1230 TTTCACTTTCACACAGAGTAGTGTGATCATCACTGACTGCTCAACAGTTGATTCCA 1289
Db 1193 TTTCACTTTTAAACAGGAATTAGATGGAGCGCCCCCTGAACTGCTTCTTAAGCTCATCCA 1252
QY 1290 GACCATATCAAGAGACAA 1307
Db 1253 GAGCATGTCAGCGGCGAA 1270
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 10:16:02 ; Search time 8631.11 Seconds
(without alignments)
7664.793 Million cell updates/sec

Title: X94939
Perfect score: 1738
Sequence: 1 AAGAAAGAGAAAGAGAGA.....ACAAAAA.....1738

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gssi.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	702.4	40.4	1409	3	CNSOABFT
2	700.8	40.3	1461	3	CNSOAB1V
3	676.8	38.9	1745	3	AY106255
4	663	38.1	1197	9	CL957492
5	634	36.5	1666	3	AY104068
6	630.6	36.3	689	1	AV821208
7	623.4	35.9	1967	3	AY103545
8	611.8	35.2	1638	3	CNS09YSF
9	607	34.9	627	1	AV439542
10	600.4	34.5	665	6	CAY781809
11	591.6	34.0	1752	3	AY108486
12	585.4	33.7	1870	3	CNSOABOL
13	581.4	33.5	2295	9	CL964803
14	580.2	33.4	887	6	CD574542
15	579.8	33.4	924	7	CK266410
16	577	33.2	1604	3	CNSOAPT
17	571.4	32.9	932	7	CV290871
18	570.4	32.8	1275	9	CL963186
19	569.6	32.8	910	7	CK290108
20	568.2	32.6	829	6	CB971865
21	558.6	32.1	1667	3	CNS0A5F6
22	550.8	31.7	566	1	AV535992
23	545.4	31.4	790	7	CO107864
24	543.2	31.3	560	1	AV781534

25	540	31.1	853	7	CK286080	CK286080	EST748802
26	540	31.1	1810	3	CNSOABFT	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
27	532.4	30.6	2036	3	CNSOABFT	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
28	527.8	30.4	963	7	CK286429	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
29	527.4	30.3	821	6	CB894470	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
30	527.4	30.3	952	7	CK289285	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
31	525.2	30.2	944	7	CK290066	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
32	517.4	29.8	551	1	AV526323	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
33	514.2	29.6	535	1	AV527913	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
34	512.2	29.5	789	7	CO120041	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
35	510.2	29.4	936	7	CK296951	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
36	509.2	29.3	1692	3	CNSOAF5S	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
37	506	29.1	757	7	CK319050	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
38	504.4	29.0	530	1	AV441767	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
39	503.8	29.0	727	7	CO083924	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
40	498.2	28.7	876	7	CF208184	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
41	497	28.6	517	1	AV821730	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
42	494.6	28.5	840	4	BM779604	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
43	492.8	28.4	919	7	CK273361	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
44	491.4	28.3	929	7	CK283056	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis
45	489.8	28.2	934	7	CK266742	Arabisopsis thaliana Full-length cDNA Complete sequence from clone	Arabisopsis

ALIGNMENTS

RESULT 1
LOCUS CNSOABFT 1409 bp mRNA linear HTC 06-FEB-2004
DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequence from clone
Arabisopsis thaliana (chale cress).
ACCESSION BX815323
VERSION BX815323.1 GI:42471412
KEYWORDS HTS; GSLT cDNA.
SOURCE Arabidopsis thaliana (chale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 1409)
AUTHORS Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Queirer,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1409)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information Center for Protein Sequences) . 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length
http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
Location/Qualifiers
1. .1409
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FEATURES

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/mol_type="mRNA"
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Matches 859; Conservative	0; Mismatches 261; Indels 0; Gaps 0;
QY	202 TGCTGATGATAGAGGATCCCTGCTGTGTAGTTGATGGACATGATCAAGTCACTGGTC 261
Db	121 TGGATTCTGATAGGAAATGCTGACAGCTGTTATTGAGGGAATGACGCTGTTACTGGTC 180
QY	262 ATATTATTTCCACACAAATCGGTGGCAAAATGGTGAAACCAACAGACAAATTAGTTACA 321
Db	181 ATATATTTTCCACTACTATTGGAGGCAAAACCGCAACCAAGCAGACATATTAGTTACA 240
QY	322 TGGCGGAGCGAGTTGTTGGTACAGGCTCGTTCCGGATCGTTTCCAGCAAAATGTTGG 381
Db	241 TGGCTGAGCGGTTGTTGGACAGGTTCAITCGGATGTTGTTTTCAGGCGAATGCTTGG 300
QY	382 AGACTCGAGAAACCGTGGCGATAAAGAGTTTTCGAAGATAGAAATCAAGAACCGAG 441
Db	301 AAACCTGGAGATCAGTAGCCATTAAAGAGTCTTTCGAAGATCGACCTATAAAACCGTG 360
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QY	682 TTTGTACAGAGATCTAAAGCTCAAACTCTCTGTTGATCTCTTACTCATCAAGTCA 741
Db	601 TTTGCCACAGAGATGTGAACCAAAATCTTGTGTTGATCCCTTGAACCATCAGTTA 660
QY	742 AAATCTGTGACTTTGGCAGTGGGAAACAGCTCGTTAAAGTGTAACCAAAATTTCTTACA 801
Db	661 AGCTGTGTGATTTTGAAGTGCAAAAGTATTGGTCAAGGTGAACCAACATATCATATA 720
QY	802 TCTGCTCAGATTTCTACCGTGACCCGAGCTCATATTGGTGCACATGAGTACACAACTT 861
Db	721 TCTGCTCCCGCTTATTATCGTGCTCCAGAACTGATCTTTGGCGCCACAGAGTATACAGCAT 780
QY	862 CTATTGATATCTGCTGCTGTTGTTCTTCTGCTGAGCTTCTTCTTGGTCAAGCAATTAT 921
Db	781 CCATAGATATATGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 840
QY	922 TCCCGGAGAAAATGCTGTGGATCAGCTCGTGGAAATTAATAAGTTCTTGTGTACCA 981
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Db	901 CTCGTGAAGAAAATTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
QY	1042 AGCCCATCTCGCAAGATCTTCCACAAAAGATGCCCCAGAGCGGTTGATTGG 1101
Db	961 AAGCTACCCCTTGGCAAGATGTTTTCATTAAGCGATGCTTCCAGAGCAATGAGACTTG 1020
QY	1102 CATCAAGGCTGCTTCAATCTCTCAAGTCTAAGATGCAAGCGCTCGAAGCTTGTGCAC 1161

Db	1021 CATCTCGGCTTCTTCAATATTCACCAAGTCTACGCTGCACATGCTCGAAGCATGTGCTC 1080
QY	1162 ATCCGCTTCTTTCATGAACTCAGAGAACCAAAACGCTCTTTTACCAATGTCAGCGCTCTCC 1221
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QY	1222 CGCTCTCTCTTCAACTTCAAAAGAGTGTGATGATCATCACTGAACTGGTCAACAAGT 1281
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QY	1282 TGATTCAGACCATATCAAGAGACAATTTGGGTCTTAAGCTT 1321
Db	1201 TAATACCTGAGCATGTGAGACGACAAATGAGCACAGGATT 1240
RESULT 2	
CNSOABIV	1461 bp mRNA linear HFC 06-FEB-2004
LOCUS	Arabidopsis thaliana Full-length cDNA Complete sequence from clone
DEFINITION	GSLTSL51ZG09 of Silique of strain col-0 of Arabidopsis thaliana
ACCESSION	EX817800
VERSION	EX817800.1 GI:42471112
KEYWORDS	HTC; GSLT cDNA.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS	Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, P., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.
TITLE	Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1461)
AUTHORS	Genoscope.
JOURNAL	Direct Submission
COMMENT	Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr) The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., URV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_Full length http://www.genoscope.cns.fr/cgi-bin/ggb?ggb?source=Arabidopsis.
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Matches 858; Conservative	0; Mismatches 262; Indels 0; Gaps 0;

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RESULT 5
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 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AY104068 1666 bp mRNA linear HTC 16-OCT-2002
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 AY104068
 AY104068.1 GI:21207146
 HTC.
 Zea mays
 Zea mays
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 1666)
 Hayney, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,
 Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
 Maize Mapping Project/DuPont Consensus Sequences for Design of
 Overgo Probes
 Unpublished (2002)
 Coe, E.H.
 Direct Submission
 Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
 If you are interested in getting corresponding physical clones,
 these are publicly available from ZmDB and may be found by BLAST
 searching at MSL, maizeimap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat
 Schnable, Iowa State, then clones may be requested from ZmDB:
 www.zmdb.iastate.edu.

FEATURES
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overgo addressing of BACs in conjunction with the Maize
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Db      1220  CGCCTACCAACGCGCGCGTTCCTCGCTCTTTAACTTCAAGCACGAACCTAGCAAT 1279
Qy      1257  TCATCACTGGAAGTGTCAACAAGTTGATTCAGACCATATCAAGAGACAATTGGGTCTA 1316
Db      1280  GCCTCTCCGAGACCTCGTCAGCAGGCTTGTCGCGAGCACATTAGACGGCAGATCGGTGTC 1339
Qy      1317  AGCTTCTTGA 1326
Db      1340  AACTTCGGGA 1349

RESULT 6
LOCUS   AV821208
DEFINITION AV821208 RAFL2 Arabidopsis thaliana cDNA clone RAFL02-10-D23 5',
mRNA sequence.
ACCESSION AV821208
VERSION   AV821208.1 GI:19863227
KEYWORDS EST.
SOURCE   Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 689)
AUTHORS Seki,M., Naruseaka,M., Iehida,J., Kamiya,A., Satou,M., Nakajima,M.,
Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y.,
Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.
and Shinozaki,K.
TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: msek@rtc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al., 1998). This clone is in a
modified pBluescript vector as a SstI/XhoI insert. Please visit our
web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for
further details.
FEATURES             Location/Qualifiers
     source           1..689
                     /organism="Arabidopsis thaliana"
                     /mol_type="mRNA"
                     /db_xref="taxon:3702"
                     /clone="RAFL02-10-D23"
                     /dev_stage="rosette plants"
                     /lab_host="SOLR"
                     /clone_lib="RAFL2"
                     /notes="Site_1: SstI; Site_2: XhoI"

ORIGIN
Query Match      36.3%; Score 630.6; DB 1; Length 689;
Best Local Similarity 96.3%; Pred. No. 1.8e-155;
Matches 664; Conservative 0; Mismatches 22; Indels 2; Gaps 2;

Qy      32  ATGCTCTTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTA 90
Db      2  ATGCTCTTGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTA 61
Qy      91  TCGCCCAATGATCATGACCAACCAACTGATTGAACTCATTTGCTCTCTCTCTCTCTCTCA 150
Db      62  TCGCCCAATGATCATTACCAACCAACTGATTGAACTCATTTGCTCTCTCTCTCTCTCTCA 121
Qy      151  ATCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 210
Db      122  ATCCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 181
Qy      211  ATAAGGAGATGCCTGCTGTGTAGTTGATGGACATGATCAAGTCACTGGTGCATATTATTT 270

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Db      182  ATAAGGAGATGCCTGCTGTGTAGTTGATGGACATGATCAAGTCACTGCTCATATTATT 241
Qy      271  CCACCACAATCGGTGGCAAAAATGGTGAACCAAAAACAGACAATTAGTTACATGGCGGAGC 330
Db      242  CCACCACAATCGGTGGCAAAAATGGTGAACCAAAAACAGACAATTAGTTACATGGCGGAGC 301
Qy      331  GAGTTGTTGGTACAGGCTCGTTTCGGGATCGTTTTTCCAAGCAAAAATGTTTGGAGACTGGAG 390
Db      302  GAGTTGTTGGTACAGGCTCGTTTCGGGATCGTTTTTCCAAGCAAAAATGTTTGGAGACTGGAG 361
Qy      391  AAACCGTGGCGATAAAGAGGTTTTTCAAGATAGAGATAACAAGAACCCAGAACCTTCAGT 450
Db      362  AAACCGTGGCGATAAAGAGGTTTTTCAAGATAGAGATAACAAGAACCCAGAACCTTCAGT 421
Qy      451  TGATCGCTGTGATGATCATCCGAATGGTTGTTGTTGTTGAAGCATTCCTTCTTTCCACTA 510
Db      422  TGATCGCTGTGATGATCATCCGAATGGTTGTTGTTGTTGAAGCATTCCTTCTTTCCACTA 481
Qy      511  CAGAGAAAGACGAGCTTTTCTTGAATCTGGTATGGAGTATGTCCTCGAGAGACGTTCTATC 570
Db      482  CAACTTAAGACGAGCTTTTCTTGAATCTGGTATGGAGTATGTCCTCGAGAGCTTGTATC 541
Qy      571  GA-GTTCTGAACATTTATAGTAGTCAAAACCAAGAAATCCCTCTTGTCTATGTTAAACTT 629
Db      542  GAGGTTCTGAACATTTATAGTAGTCAAAACCAAGAAATCCCTCTTGTCTATGTTAAACTT 601
Qy      630  TACAGTTATCAGATCTTCCGGGACTTGTCTTACATTCACATTCACATTCGCGGAGTTTGTAC 689
Db      602  TACATGTATCAGATCTTTCGGGACTTGTCTTACATTCACATTCACATTCGCGGAGTTTGTAC 661
Qy      690  AGAGATCTAAAGCTCAAAATCTTCTGG 717
Db      662  ANAGATCTAAAGCTCAAAATCTTCTGG 689

RESULT 7
LOCUS   AY103545
DEFINITION Zea mays P00153236 mRNA sequence.
ACCESSION AY103545
VERSION   AY103545.1 GI:21206623
KEYWORDS HTC.
SOURCE   Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1967)
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1967)
AUTHORS Coe,E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of
Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones,
these are publicly available from ZmDB and may be found by BLAST
searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
maize cDNA sequences is either Virginia Walbot, Stanford or Pat
Schabbe, Iowa State, then clones may be requested from ZmDB:
www.zmdb.iastate.edu.
FEATURES             Location/Qualifiers
     source           1..1967
                     /organism="Zea mays"
                     /mol_type="mRNA"
                     /db_xref="MaizeDB:638897"
                     /db_xref="taxon:4577"
                     /clone_lib="Maize Mapping Project/DuPont Consensus

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Library"

/note--this sequence is part of a project of EST assemblies resulting from the application of public configs to seed DuPont configs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"

ORIGIN

Query Match 35.9%; Score 623.4; DB 3; Length 1967;
Best Local Similarity 73.4%; Pred. No. 1.9e-153;
Matches 811; Conservative 0; Mismatches 291; Indels 3; Gaps 1;

207	Qy	GATGATTAAGGAGATGCCGTGCTGTGTAGTTGATGGACATGATCAAGTCACTGGTGTATATT	266
456	Db	GATGATTAAGGAAGTTGAAGCAACCATTAATTAAATGGGAAGGCACTGAAACTGGGCACATA	515
267	Qy	ATTTCACACCAATTCGGTGGCAGAAATGGTGAACCAAAACAGACAAATTAGTTTACATGGCG	326
516	Db	ATTGTCACCACTACTGGTGGCAGAGATGGTCAACAAACAGACAGTGAAGTACTATGGCT	575
327	Qy	GAGCGAGTTGTTGGTACAGGCTCGTTTCGGGATCGTTTTCCAGCAAAATGTTTGGAGACT	386
576	Db	GAGCGCATTTGATGTCGAAGTTCTTTTGGGATCGTCTTCCAGGCCAAGTGTTTGGAAACG	635
387	Qy	GGAGAAACCGTGGCGATAAAGAGGTTTTGCAAGATAGAAATCAAGAACCGAGAACTT	446
636	Db	GGTGAGACTGTGCCATAAAGAGGTTCTTCAAGACAAGCGTTTACAAGAACCGGAACTG	695
447	Qy	CAGTTGATCGGTGTGATGGATCATCCGAATGTGGTTTTGTTTGAAGCATTGCTTCTTTTCG	506
696	Db	CAGACCATGGCCCTTCTTGACCACCCTAAATGTTGTGCTTTGAAGCATTGCTTCTTTTCA	755
507	Qy	ACTACAGAGAAAGACGAGCTTTTCTGCAACTTGTGTTATGGAAGTATGTCCCTGAGACGTTG	566
756	Db	ACTACTGAGAAGAGTATGAGCTTTATCTGAACCTTGTTCCTTGGATGATGTTCCGAGACAGTT	815
567	Qy	TATCGAGTTCTGAAACATTAATAGTAGTGTCAACCAAGAAATGTCCTTGTCTATGTTAAA	626
816	Db	CATCGAGTTGTGAAACATCAACAAGATGCACCAACGCATGCCACTTAATTTATGTGAAG	875
627	Qy	CTTTACAGTTATCAGATCTTCGGGGACATTGCTTTACATTTACAGTTGCCCAGGAGTTTGT	686
876	Db	CTTTTATATGTAACAGATATGTAGAGCATTTGGCTTTACATTTATGTTGATCTATCGGTGTCTGC	935
687	Qy	CACAGAGATCTTAAGCGCTCAAAATCTTCTGGTTGATCCTCTTACTCATCAAGTCAAAATC	746
936	Db	CACAGAGATTAATAGCCACAAAATCTTCTGGTGAACCAACACCCACAGCTTTAAANA	995
747	Qy	TGTGACTTTTGGCAGTGCAGAAACAGCTCGTTAAAGGTGAACCAAAACATTTCTTACATCTGC	806
996	Db	TGTGACTTTTGGTAGTGCAGAAAGTTCTGTCAGGGGGGAAACCAACATATCATACATCTGC	1055
807	Qy	TCACGATTTACCGTGCACCCGAGCTCATATTTGGTGGCACTGAGTACACAACTTCTATT	866
1056	Db	TCGCGATACTATAGGGCTCCAGAGCTCATATTTGGTGGCACTGAGTATACCAACGCGATT	1115
867	Qy	GATATCTGCTGCTGCTGTGTTCTTGTCTGAGCTTCTTCTGGTCCAGGCATTAATCCCC	926
1116	Db	GACATTTGGTCTGCTGGAATGTTTCTTGTGAGCTTATGCTAGGGCAGCCCTTGTGTTCCG	1175
927	Qy	GGAGAAATGCTGTGGATCAGCTCGTGGAAATTAATAAGTTCTTGGTACACCAACTCGA	986
1176	Db	GGTGAAGTGGTGTGGACCAACTGTTTGAATTCATCAGGTCTTCGGTACGCCAACAGG	1235
987	Qy	GAAGAAATCCGTTGTATGAATCCCAACTACACAGATTTCAAGTTTCCACAGATAAAGGCC	1046
1236	Db	GAAGAAATTAATGTCATGAACCCAAATTAACACAGAGTTTAAGTTTCCACAAAATCAAAGCA	1295
1047	Qy	CATCCCTGGCACAAGATCTTCCACAAAAGATGCCCCAGAGCGGTTGATTTGGCATCA	1106
1296	Db	CACCCATGGCAAGGTATTTCACAAAGAGATGCCGACAGAGCTGTGATCTGTGCTCT	1355

Query Match 35.2%; Score 611.8; DB 3; Length 1638;
Best Local Similarity 72.5%; Pred. No. 2.1e-150;

Qy	1107	AGCGTGTCTCAATCTCTCAAGCTTAAGATGCAAGCGCTCGAAGCTTGTGCACATCCG	1166
Db	1356	CGGCTACTCGAGTACTCCCAAACTCTGAGATGCACTGCTATGGAGGCACCTTGTTCACCCA	1415
Qy	1167	TTCTTTTGATCAACTCGAGAGACCAAGCGCTGTTTACCAAACTCGAGCGCTCTCCCGCCT	1226
Db	1416	TTCTTTTGATGAGCTTGCAGATCTCTAATCTCGCGCTTCCAAATGGTCGCTTTTGGCCACCA	1475
Qy	1227	CTCTTCAACTTTCAA---ACAAGAAGTAGCTGGATCATCACTGAACTGGTCAACAAGTTG	1283
Db	1476	CTATTCAATTTCAAGCCTCAGCAACTTAAGAGAGTCCCATCAGACATTTGTTCGGAATTG	1535
Qy	1284	ATTCGAGACCATATCAAGACAAAT	1308
Db	1536	GTTCACGAAATCGAAGAGCAAT	1560

RESULT 8
CNS09YSF
LOCUS
DEFINITION
CNS09YSF 1638 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTUS9IZE05 of Adult vegetative tissue of strain col-0 of
Arabidopsis thaliana (thale cress).

ACCESSION BX831446
 VERSION BX831446.1 GI:42455013
 KEYWORDS HTC; GSJLT CDNA.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS
1 (bases 1 to 1638)
Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
TITLE
Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome

**JOURNAL
REFERENCE**
2 (bases 1 to 1638)

AUTHORS
Genoscope.
TITLE
Direct Submission
JOURNAL
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
BP 131 91006 EVRY cedex - FRANCE (E-mail : segraf@genoscope.cns.fr
- web : www.genoscope.cns.fr)

COMMENT

Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externes/sequences/Banque_Projet_EF/Full_length

FEATURES
source 1. .1638
Location/Qualifiers
<http://www.gnoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis>.

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/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Col-0"
/db_xref="taxon:3702"
/clone="GSLRLS91ZE05"
/tissue_type="Adult vegetative tissue"
/plasmid="pCMVSPORT 6"
complement(1..1638)
/gene="At5g26751"

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ORIGIN

Query Match
Best Local


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Db      327 GAACCTAAAGGATCTCTGCAAGACAACTACTTTTATATATATAATGACCATACAC 268
QY      1396 GAGCCACAAGGTCGTAGTTGAAGGCAAAACGTGGAGGACACAATCAAAAGTTTCTCTCT 1455
Db      267 GAGCCACAAGGTCGTAGTTGAAGGCAAAACGTGGAGGACACAATCAAAAGTTTCTCTCT 208
QY      1456 CAAACTCGTTTCAGACAAAGCCAGCTGCTAGCAAAACCAACT-ACCCAATCTGCGAAGAC 1514
Db      207 CAAACTCGTTTCAGACAAAGCCAGCTGCTAGCAAAACCAACT-ACCCAATCTGCGAAGAC 148
QY      1515 AAAAACTCTCCAGTGTGTATCTGCTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1574
Db      147 AAAAACTCTCCAGTGTGTATCTGCTTATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 88
QY      1575 ACAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1634
Db      87 ACAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 28
QY      1635 GAAGTTTTTTTATATAGTAAGTTGG 1661
Db      27 GAAGTTTTTTTATATAGTAAGTTGG 1

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RESULT 10
CA781809
LOCUS 051801AF Infected Arabidopsis Leaf Arabidopsis thaliana cDNA, mRNA
DEFINITION CA781809
ACCESSION CA781809.1 GI:26019845
VERSION
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS 1 (bases 1 to 665)
Lundsgaard, M., Emmeren, J., Nielsen, K.L., Wilson, I., Somerville, S. and Welinder, K.G.
TITLE EST sequencing of Erysiphe cichoracearum infected Arabidopsis plants
JOURNAL Unpublished (2002)
COMMENT Contact: Karen G. Welinder
Institut for bioteknologi
Aalborg Universitet
Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kgw@bio.au.dk.

FEATURES
source
1. .665
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/dev_stages="plant 3 weeks old, three days post infection"
/clone_lib="Infected Arabidopsis Leaf"
/note="Organ: Leaf; Vector: pBluescript; Mixed cDNA library of Arabidopsis and E. cichoracearum infected leaf from three weeks old Arabidopsis plants. Plants were harvested 3 days after infection and mRNA oligo dt selected."

ORIGIN
Query Match 34.5%; Score 600.4; DB 6; Length 665;
Best Local Similarity 95.8%; Pred. No. 1.8e-147;
Matches 638; Conservative 0; Mismatches 26; Indels 2; Gaps 2;

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QY      373 AATGTTTGAGACTCGAGAACCGTGGCATAAAGAGTTTTCGAAGATAGAGATACA 432
Db      1 AATGTTTGAGACTCGAGAACCGTGGCAT-AAGAGGTTTTCGAAGATAGAGATACA 59
QY      433 AGAACCGAGAACTTCAGTTGATGCGGTGATGATCATCCGAATGCTGTTGTTGAAGC 492

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Db      60 AGAACCGAGAACTTCAGTTGATGCGGTGATGATCATCCGAATGCTGTTGTTGAAGC 119
QY      493 ATTGCTTCTTTTGAACACGAGAGCTTTTCTTGAACCTTGGTTATGGAGTATG 552
Db      120 ATTGCTTCTTTTGAACACGAGAGCTTTTCTTGAACCTTGGTTATGGAGTATG 179
QY      553 TCCCTGAGACGTTGATCGAGTTCTGAAACATTAAGTAGTGCACAAACCAAGAAATGCCTC 612
Db      180 TCCCTGAGACGTTGATCGAGTTCTGAAACATTAAGTAGTGCACAAACCAAGAAATGCCTC 239
QY      613 TTGCTATGTTAAACCTTTACAGTTATCAGATCTTCCGGGAGCTT-GCTTTACATTCACAGT 671
Db      240 TTGCTATGTTAAACCTTTACAGTTATCAGATCTTCCGGGAGCTTGGCTTACATTCACAT 299
QY      672 TGCCGGGAGTTTGTACAGAGATCTAAAGCCTCAAAATCTTCTGGTTGATCCTCTTACT 731
Db      300 GTTGCTGGAGTTTGTACAGAGATCTAAAGCCTCAAAATCTTCTGGTTGATCCTCTTACT 359
QY      732 CATCAAGTCAAAATCTGTGACTTTGGCAGTGGGAAACAGCTGCTTAAAGGTTGAACCAAC 791
Db      360 CATCAAGTCAAAATCTGTGACTTTGGCAGTGGGAAACAGCTGCTTAAAGGTTGAACCAAC 419
QY      792 ATTCTTACATCTGCTCAGATTTCTACCGTGCACCGAGCTCATATTTGGTCCCACTGAG 851
Db      420 ATTCTTACATCTGCTCAGATTTCTACCGTGCACCGAGCTCATATTTGGTCCCACTGAG 479
QY      852 TACACAACCTTCTATTGATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 911
Db      480 TACACAACCTTCTATTGATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 539
QY      912 CAGCCATTATTTCCCGGAGAAAATGCTGTGATCAGCTGCTGCGGAAAATTTAAAGTTCTTT 971
Db      540 CAGCCATTATTTCCCGGAGAAAATGCTGTGATCAGCTGCTGCGGAAAATTTAAAGTTCTTT 599
QY      972 GGTACACCAACTCGAGAGAAAATCCGTTGATGATCCCACTACACAGATTTCAAGTTTC 1031
Db      600 GGTACACCAACTCGAGAGAAAATCCGTTGATGATCCCACTACACAGATTTCAAGTTTC 659
QY      1032 CCACAG 1037
Db      660 CCACAG 665

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RESULT 11
AY108486
LOCUS AY108486
DEFINITION Zea mays P0107502 mRNA sequence.
ACCESSION AY108486
VERSION AY108486.1 GI:21211564
KEYWORDS HTC.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 1752)
AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whiteitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1752)
AUTHORS Coe, E.H.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB:


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Db      422  CATTGATAGATTGAGCAATACAGCAGTGCATAATCAGAGATGCCCTCATATATGT 481
Qy      623  TAAACTTTACAGTATCAGATCTTCGGGGAGCTTGCTTACATTCACAGTTGCCCGGAGT 682
Db      482  GAAACITTTATACGTACAGATTTTCAGGGGCTGGCTTACATCCACACATGTTCTCGAGT 541
Qy      683  TTGTACAGAGATCTAAAGCTCAAAATCTTCGGTTGATCTCTTACTCATCAAGTCAA 742
Db      542  TTGCCATAGGGATTGAAGCCTCAAAACCTTTTGGTTGATCTCTTACTCACAGGTTAA 601
Qy      743  AATCTGTGACTTTGGCAGTGCAGAACAGCTCGTTAAAGGTGAACCAAAATTTCTTACAT 802
Db      602  GATTGTGATTTTGGAGTGGCAAAACAGCTGATTCGTGGAGAGCAAAATATATACATAT 661
Qy      803  CTGCTCACGATTTACCGTGCAACCCGAGCTCATATTTTGGTGCCACTGAGTACACAACTTC 862
Db      662  ATGTTACAGTTCTATCGGCTCGGAACCTATATTTGGAGCTACAGATATACAACTTC 721
Qy      863  TATTGATATCTGCTGCTGTTGTTGTTCTGCTGAGCTTCTTCTTGGTCAACCAATTATT 922
Db      722  AATTGATATATGCTCAGCTGGTTGTGCTTGCAGCTTCTTTGGGCGAGCAATTATT 781
Qy      923  CCCCAGAGAAATGCTGTGATGATGAATCCCAACTACACAGATTTCAAG 1028
Db      782  TCTGAGAGAAATGCGTGTGATGATGAATCCCAAAATATATACCGATTTAGG 887
Qy      983  TCGAGAGAAATCCGTTGTATGAATCCCAACTACACAGATTTCAAG 1028
Db      842  TCGTGAAGAAATCGTTGTATGAATCCCAAAATATATACCGATTTAGG 887

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RESULT 15

CK266410

LOCUS

EST712488 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone POAC457 5' end, mRNA sequence.

CK266410

VERSION

KEYWORDS

SOURCE

ORGANISM

Solanum tuberosum (potato)
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.

1 (bases 1 to 924)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.

Generation of ESTs from abiotic stressed potato tissue

Unpublished (2003)

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@igr.org

Clones can be requested from the University of Arizona Genomics

Institute via <http://genome.arizona.edu/orders/>

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

1..924

/organism="Solanum tuberosum"

/mol_type="mRNA"

/cultivar="Kennebec"

/db_xref="taxon:4113"

/clone="POAC457"

/tissue_type="abiotic stress treated leaf and root tissue"

/lab_host="PH108-Tona"

/clone_lib="potato abiotic stress cDNA library"

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;

supplier: Solanum tuberosum var. Kennebec plants were

grown from cuttings on a 16hr light/8 hr dark cycle at 25

C for 3-4 weeks. Abiotic stress conditions were applied to

four separate sets of plants. Set 1 involved saturation of

the soil with 150 mM NaCl and tissues were harvested at

following application of the salt stress (leaves: 2hr,

6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

ORIGIN

```

Query Match      33.4%; Score 579.8; DB 7; Length 924;
Best Local Similarity 76.9%; Pred. No. 5.5e-142;
Matches 707; Conservative 0; Mismatches 212; Indels 0; Gaps 0;

346  GCTCGTTCGGGATCGTTTCCAAAGCAAAATGTTTCGAGACTGGAGAAACCGTGGCGATAA 405
Db      1  GGTCTTTTGGGATAGTGTTCAGGCAAAATGTTTCGAAACTGGAGAGACTGGGCCATAA 60

406  AGAAGGTTTTCGAAGATAGAAGATACAAGAACCGAGAACTTCAGTTGTATGCTGTGATGG 465
Db      61  AGAAGGTTTTCAGGACAAAGCGGTATATAAACCGTGAACACTACAACATGATGCCCTTATGG 120

466  ATCATCCGAATGTGGTTTGTGTAAGCAATGCTCTTTTCGACTACAGAGAAAGACGAGC 525
Db      121  ATCACCCTCAATGTCTATTAAGCACTGCTCTTTTCCACGACTAGTAGAGATGAGC 180

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Db      481  CAGAACTCATATTTGGTGGCCACAGAAATACAACATCAATGATATTTGGTCAGCAGGCT 540

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Job time : 8635.11 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 05:27:02 ; Search time 11439.2 Seconds
(without alignments)
6929.914 Million cell updates/sec

Title: X94938
Perfect score: 1636
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Scoring table: IDENTITY_NUC
Gapop 10_0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	975.6	59.6	1572	8 AF019927	Arabidops
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9	939.8	57.4	1255	8 AY051053	Arabidops
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ALIGNMENTS

RESULT 1
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DEFINITION A.thaliana mRNA for shaggy-like kinase dzeta.
ACCESSION X94938
VERSION X94938.1 GI:1161509
SOURCE ASK dzeta gene; serine/threonine kinase; shaggy-like kinase dzeta.
KEYWORDS Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1
AUTHORS Dornelas,M.C., Schwebel-Dugue,N., Thomas,M., Lecharny,A. and Kreis,M.
TITLE Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939 and X99696) (PGR97-008)
JOURNAL Plant Physiol. 113, 306-306 (1997)
REFERENCE 2 (bases 1 to 1636)
AUTHORS Dornelas,M.C.
TITLE Direct Submission
JOURNAL Submitted (10-JAN-1996) M.C. Dornelas, UNIVERSITE de Paris-Sud, Institut de Biotechnologie des Plantes, Centre de Recherches sur les Plantes, URA 1128, Biol.du Devel.des Plantes, Bat.630, F-91405 ORSAY Cedex, FRANCE
COMMENT Corresponding genomic sequence: Y09300.
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AUTHORS

Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

TITLE
JOURNAL
REFERENCE

Arabidopsis cDNA clones

AUTHORS

Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.

Direct Submission

TITLE
JOURNAL

Submitted (08-APR-2002) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bower, J., Chang, E., Dale, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.

Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES

source

Location/Qualifiers

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Matches 1550; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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RESULT 3

LOCUS

DEFINITION Arabidopsis thaliana putative shaggy protein kinase dzeta
 (At2g30980) mRNA, complete cds.

ACCESSION

VERSION AY064020.1 GI:17381127

KEYWORDS

SOURCE Arabidopsis thaliana

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids;
 1 (bases 1 to 1566)

REFERENCE

AUTHORS

Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
 Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
 Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
 Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
 Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
 Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,
 Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE

JOURNAL

REFERENCE

AUTHORS

Yamada,K., Banh,J., Banno,F., Chang,E., Dale,J.M., Goldsmith,A.D.,
 Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C.,
 Yamamura,Y., Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H.,
 Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A.,
 Karlin-Neumann,G., Kawai,J., Kim,C., Koesema,E., Lam,B., Lin,J.,
 Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
 Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A.,
 Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE

JOURNAL

COMMENT

Submitted (19-NOV-2001) Plant Gene Expression Center, 800 Buchanan
 Street, Albany, CA 94710, USA
 RIKEN Genomic Sciences Center
 collection and clustering of RAPL cDNAs (RAPL cDNA : 'RIKEN
 Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J.,
 Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
 Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PEGC (SSP) Consortium members carried out the
 sequencing and annotation of the RAPL cDNAs: Yamada,K., Banh,J.,
 Banno,F., Chang,E., Dale,J.M., Goldsmith,A.D., Lee,J.M.,

Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C.,
 Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T.,
 Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C.,
 Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A.,
 Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PEGC) and Seki,M. (RIKEN GSC) contributed equally to
 this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PEGC)
 contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis
 genome submitted to GenBank.

FEATURES

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3'UTR

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ACCESSION AY087542
VERSION AY087542.1 GI:21406280
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 1503)
AUTHORS Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
TITLE Full-length messenger RNA sequences greatly improve genome
annotation
JOURNAL Genome Biol. 3 (6), RESEARCH0029 (2002)
MEDLINE 22088475
PUBMED 12093376
REFERENCE 2 (bases 1 to 1503)
AUTHORS Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
TITLE Full-length cDNA from Arabidopsis thaliana
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 1503)
AUTHORS Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
TITLE Direct Submission
JOURNAL Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA
COMMENT This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to TIGR and Genbank. The following quality assessment of
this set was done by comparison with known proteins: two percent of
the clones are estimated to be 5'-truncated; less than one percent
are 3'-truncated; approximately two percent represent alternative
splice variants, including unspliced introns and spliced exons; one
percent may contain premature stop codons; five percent may have
frame shifts in a coding region. A sequence is considered to be
5'-truncated if it lacks the translation initiation start (ATG). A
sequence is considered to be 3'-truncated if it lacks the
C-terminal end of the encoded protein. Please note that these cDNA
sequences are derived from the Ws or Laer ecotypes and therefore
may contain polymorphisms when compared to sequences from Col-0.
Genet carried out the library production and sequencing of the
full-length clones. Ceres, Inc. carried out the clustering of the
5' sequences, selection of clones, and sequence assembly.

FEATURES

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LOCUS			
DEFINITION	Arabidopsis thaliana putative shaggy protein kinase dzeta (At2g30980) mRNA, complete cds.		
ACCESSION	AY096698.1	GI:20465726	
VERSION			
KEYWORDS	FLI CDNA.		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
REFERENCE			
AUTHORS	Yamada, K., Barth, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.		
TITLE	Arabidopsis Open Reading Frame (ORF) Clones		
JOURNAL	Unpublished		
REFERENCE			
AUTHORS	Yamada, K., Barth, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-APR-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA		
COMMENT	The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN		

Arabidopsis Full-Length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinzaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAPL cDNAs: Yamada, K., Banh, J., Chan, M. M., Chang, C. H., Chang, E., Dale, J. M., Deng, J. M., Goldsmith, A. D., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Toriumi, M., Wu, H. C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B., Lin, J., Meyers, M. C., Miranda, M., Nguyen, M., Palm, C. J., Shinn, P., Southwick, A., Davis, R. W., Ecker, J. R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinzaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

FEATURES

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3' UTR

ORIGIN

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Matches 1266; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 225 GGC AAAATGTTGAACCTTAAACAGACCAATGATTACATGGCGCGAAGCTGTGTTGGAACA 284
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RESULT 6
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LOCUS
DEFINITION Arabidopsis thaliana GSK3/shaggy-like protein kinase (GSK1) mRNA,

1572 bp mRNA linear PLN 14-MAY-1999

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1 (bases 1 to 1572)	576
Piao,H.L., Pih,K.T., Lim,J.H., Kang,S.G., Jin,J.B., Kim,S.H. and	551
Hwang,I.	611
An Arabidopsis GSK3/shaggy-like gene that complements yeast salt	696
stress-sensitive mutants is induced by NaCl and abscisic acid	671
Plant Physiol. 119 (4), 1527-1534 (1999)	756
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2 (bases 1 to 1572)	791
Piao,H.L., Jang,H.J., Pih,K.T., Lim,J.H., Kang,S.G., Jin,J.B. and	876
Hwang,I.	851
Direct Submission	936
Submitted (18-AUG-1997) Plant Molecular Biology and Biotechnology	911
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LOCUS Arabidopsis thaliana putative shaggy kinase (At1g06390) mRNA,
DEFINITION complete cds.
ACCESSION AY035048
VERSION AY035048.1 GI:14334749
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1582)
Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K.,
Davis,R.W., Ecker,J.R. and Theologis,A.
Arabidopsis Full Length cDNA Clones
Unpublished
2 (bases 1 to 1582)
Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldsmith,A.D., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Yu,G.,
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Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M.,
Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and
Theologis,A.

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TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Submitted (03-MAY-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K., Goldsmith,A.D., Lee,J.M., Quach,H.L., Tang,C.C., Toriumi,M., Yu,G., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers

FEATURES

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RESULT 8
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DEFINITION X99696
ACCESSION X99696.1 GI:1480077
VERSION AKS iota gene; shaggy-like kinase iota.
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1
AUTHORS Dornelas,M.C., Schwebel-Dugue,N., Thomas,M., Lecharny,A. and
Kreiss,M.
TITLE Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase
Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939
and X99696) (PCR97-008)
JOURNAL Plant Physiol. 113, 306-306 (1997)
REFERENCE 2 (bases 1 to 1614)
AUTHORS Dornelas,M.C.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-1996) M.C. Dornelas, Universite De Paris-Sud
(Parisxi), Institut De Biotechnologie Des Plantes, Lab. Biol. Du
Developpement Des Plantes, Batiment 630, F-91405 Orsay Cedex,
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Best Local Similarity 77.0%; Pred. No. 4.2e-171;
Matches 1234; Conservative 0; Mismatches 343; Indels 26; Gaps 3;
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LOCUS Arabidopsis thaliana putative shaggy kinase (At1g06390) mRNA,
 complete cds.

ACCESSION AY051053

VERSION AY051053.1 GI:15293238

KEYWORDS FLI, CDNA.

ORGANISM Arabidopsis thaliana (thale cress)

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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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REFERENCE

AUTHORS

Yanada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Egtu, P.,
 Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H.,
 Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M.,
 Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and
 Theologis, A.

Arabidopsis Open Reading Frame (ORF) Clones

Unpublished

2 (bases 1 to 1255)

Yanada, K., Liu, S.X., Pham, P.K., Banh, J., Banno, F., Dale, J.M.,
 Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L.,
 Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L.,
 Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
 Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C.,
 Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M.,
 Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P.,
 Southwick, A., Tracy, S.E., Shinozaki, K., Davis, R.W., Ecker, J.R. and
 Theologis, A.

Direct Submission

TITLE

JOURNAL

Submitted (02-AUG-2001) Plant Gene Expression Center, 800 Buchanan
 Street, Albany, CA 94710, USA
 The RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAPL cDNAs (RAPL cDNA : 'RIKEN
 Arabidopsis Full-length cDNA') Seki, M., Narusaka, M., Ishida, J.,
 Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
 Hayashizaki, Y. and Shinozaki, K.

COMMENT

The Salk, Stanford, PGECC (SSP) Consortium members constructed and
 sequenced the PUNI (ORF) clones using the RAPL cDNAs: Yanada, K.,
 Liu, S.X., Pham, P.K., Banh, J., Banno, F., Dale, J.M., Goldsmith, A.D.,
 Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,

Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H.,
Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koesema, E., Lam, B.,
Lin, J., Meyers, M. C., Miranda, M., Nguyen, M., Palm, C. J., Shinn, P.,
Southwick, A., Tracy, S. E., Davis, R. W., Ecker, J. R. and Theologis, A.

Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally
to this work. Shinzaki, K. (RIKEN GSC) and Theologis, A. (SSP
/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis
genome submitted to GenBank.

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RESULT 10

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DEFINITION A.thaliana mRNA for shaggy-like kinase etha.
ACCESSION X94939
VERSION X94939.1 GI:1161511
KEYWORDS ASK etha gene; shaggy-like kinase etha.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
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Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lecharny, A. and
Kreiss, M.
Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase
Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939
and X99696) (F0897-008)

JOURNAL	Plant Physiol. 113, 306-306 (1997)
REFERENCE	2 (bases 1 to 1738)
AUTHORS	Dornelas, M.C.
TITLE	Direct Submission
JOURNAL	Submitted (10-JAN-1996) M.C. Dornelas, UNIVERSITE de Paris-Sud, Institut de Biotechnologie des Plantes, Centre de Recherches sur les Plantes, URA 1128, Biol.du Devel.des Plantes, Bat.630, F-91405 ORSAY Cedex, FRANCE
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AUTHORS	Brover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and Feldmann, K.	Qy	497	AGAGACATTGTACCGGTTTTCGAAACACTATATAGTTCAAACACGCGATGCTATCTT	556
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	Direct Submission				
TITLE	Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA	Qy	617	TGGTGTCTGCCACAGAGATATAAAACCAAAATCTTTTGGTTGATCCCAACCCATCA	676
	This clone sequence is one of 5,000 Ceres full-length cDNAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins; two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent represent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these cDNA sequences are derived from the Ws or Laer ecotypes and therefore may contain polymorphisms when compared to sequences from Col-0. Geneset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.		649	TGGAGTTTGTCAAGAGATCTAAAGCCTCAAATCTTCTGGTTGATCTCTTACTCATCA	708
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AK073725

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

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AK073725

AK073725.1 GI:32983748

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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

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Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

AUTHORS

The Rice Full-Length cDNA Consortium, National Institute of
 Agrobiological Sciences Rice Full-Length cDNA Project Team:
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashita, N., Doi, K.,
 Kiehmoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I.,
 Kojima, K., Naniwa, T., Ohneda, S., Yahagi, W., Suzuki, K., Li, C.,
 Ohtsuki, K., Shishiki, T., Foundation of Advancement of International
 Science Genome Sequencing & Analysis Group; Ohtsuki, K.,
 Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y.,
 Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
 Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
 Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J.,
 Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN;
 Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S.,
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 Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
 Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
 Yoshino, M. and Hayashizaki, Y.

Collection, mapping, and annotation of over 28,000 cDNA clones from

japonica rice

Science 301 (5631), 376-379 (2003)

22752273

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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K.,
 Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W.,
 Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T.,
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 Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M.,
 Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A.,
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 Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, I., Tomaru, A.,
 Toyota, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yanagi, W.,
 Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
 Yoshimura, A.

Direct Submission

JOURNAL

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
 Agrobiological Sciences, Department of Molecular Genetics, Head of
 Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp,
 Tel:81-29-838-7007, Fax:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica

rice.

URL : <http://cdna01.dna.affrc.go.jp/cDNA/>

NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nariakawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Tokomizo, S., Yoshimura, A., Matsuura, K. and Murakami, K.

Genome Exploration Research Group in Riken Genomic Science Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ootato, N., Ota, Y., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

FEATURES

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SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1484.4	90.7	1501	3 AAC47571	Aac47571 Arabidops
2	1478	90.3	1503	3 AAC37569	Aac37569 Arabidops
3	958.2	58.6	1567	3 AAC42073	Aac42073 Arabidops
4	775.2	47.4	1744	8 AAC57975	Aac57975 Soybean p
5	736	45.0	1657	3 AAC47997	Aac47997 Arabidops
6	733	44.8	1490	10 AAL54221	Aal54221 cDNA of w
7	733	44.8	1745	3 AAC47206	Aac47206 Arabidops
8	730.8	44.7	1143	6 AB213070	Ab213070 Arabidops
9	730.8	44.7	1143	12 ADN73384	Adn73384 Thale cre
10	722.6	44.2	1635	3 AAC41916	Aac41916 Arabidops
11	709	43.3	1621	8 ACC57970	Acc57970 Canola pr
12	705	43.1	1499	8 ACC57973	Acc57973 Soybean p
13	682.6	41.7	1653	3 AAC48014	Aac48014 Zea mays
14	667.2	40.8	1673	5 AAH47004	Aah47004 Wheat gly
15	667.2	40.8	1673	6 ABQ82534	Abq82534 Wheat gly
16	657.4	40.2	1789	3 AAC51694	Aac51694 Zea mays
17	618.4	37.8	1713	3 AAC47761	Aac47761 Zea mays
18	605.2	37.0	1849	8 ACC57962	Acc57962 Protein k
19	602.8	36.8	1824	3 AAC47763	Aac47763 Zea mays
20	602.2	36.8	1218	3 AAC48306	Aac48306 Arabidops

21	601.2	36.7	1796	3 AAC46604	Aac46604 Zea mays
22	591	36.1	1717	3 AAC38960	Aac38960 Arabidops
23	587.8	35.9	1230	6 ABZ14553	Abz14553 Arabidops
24	587.8	35.9	1716	3 AAC45767	Aac45767 Arabidops
25	582.2	35.6	1410	12 ADQ37156	Adq37156 Cell prol
26	582.2	35.6	1410	12 ADQ15740	Adq15740 Rice stre
27	582	35.6	1610	8 ACC57977	Acc57977 Rice prot
28	557.2	34.1	1814	5 AAH47001	Aah47001 Corn glyc
29	557.2	34.1	1814	6 ABQ82531	Abq82531 Maize gly
30	557	34.0	1419	3 AAC43095	Aac43095 Arabidops
31	557	34.0	1419	12 ADN72934	Adn72934 Thale cre
32	547.6	33.5	1344	3 AAC42818	Aac42818 Arabidops
33	545.4	33.3	1866	8 AAL55586	Aal55586 CDNA enco
34	544.8	33.3	1523	8 ACC57974	Acc57974 Soybean p
35	538.8	32.9	1429	5 AAH47003	Aah47003 Soy bean
36	538.8	32.9	1429	6 ABQ82533	Abq82533 Soybean g
37	529.4	32.4	1757	8 ACC57969	Acc57969 Canola pr
38	489	29.9	1654	8 ACC57971	Acc57971 Canola pr
39	485	29.6	1296	6 ABZ12869	Abz12869 Arabidops
40	485	29.6	1296	6 ADG87959	Adg87959 A. thalia
41	485	29.6	1296	12 ADN73136	Adn73136 Thale cre
42	428	26.2	1100	8 ACC57961	Acc57961 Protein k
43	402.4	24.6	2155	10 ADB58321	Adb58321 Toxicity-
44	400.8	24.5	1698	10 ADC99112	Adc99112 Human KPP
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ALIGNMENTS

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DT 18-OCT-2000 (first entry)
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KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
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OS Arabidopsis thaliana.
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PD 06-SEP-2000.
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RESULT 5
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ID AAC47997 standard; DNA; 1657 BP.
XX AC AAC47997;
DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 55886.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
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 76 CGCATGGCTGATGATAAGAGAGATGCCCTGCTGCTGATGTTGAGGACATGATCAAGTAC 135

Db 1216 AACCTAAAAGG 1227

RESULT 6
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ID AAL54221 standard; cDNA; 1490 BP.
XX AAL54221;
AC AAL54221;
XX 27-MAR-2003 (first entry)
XX cDNA of wild-type DWf12 protein.
DB DWf12; transgenic plant; plant breeding; industrial application;
KW agricultural production; gene; ss.
XX Unidentified.
OS
FH Key Location/Qualifiers
FT CDS 200..1312
FT /*tag= a
FT /product= "Protein of wild-type DWf12 locus"
XX
PN WO200292777-A2.
XX
PD 21-NOV-2002.
XX
PF 15-MAY-2002; 2002WO-US015563.
XX
PR 16-MAY-2001; 2001US-0291342P.
XX
PA (ARIZ-) ARIZONA BOARD OF REGENTS.
XX
PI Choe S, Feldmann K, Tax F;
XX
DR WPI: 2003-129285/12.
DR P-PSDB; AAO26726, AAO26727.
XX
PT New isolated DWf12 mutant polypeptide for producing transgenic plants
PT displaying altered biochemistry, structure or morphology which are useful
PT in plant breeding, in agricultural production or industrial applications.
XX
PS Example 2; Fig 2; 62pp; English.
XX
CC The invention relates to an isolated DWf12 (DWf12) mutant polypeptide.
CC The mutant polypeptide comprises at least 70 % sequence identity to the
CC amino acid sequence of the DWf12 polypeptide given in the specification
CC at positions 38-326 or 1-380, and having a mutation of at least one non-
CC conservative substitution, addition or deletion of an amino acid in a
CC region of the polypeptide corresponding to a region given in the
CC specification. The mutant DWf12 polypeptide is useful in producing
CC transgenic plants that display at least one altered DWf12 phenotype, such
CC as altered biochemistry, structure or morphology. The transgenic plant
CC can be used in plant breeding or directly in agricultural production or
CC industrial applications. The polynucleotide is useful in isolating or
CC creating other mutant cell gene alleles, in inhibiting or enhancing
CC endogenous DWf12 gene expression, and in standard diagnostic assays as
CC hybridisation probe or primer. This polynucleotide sequence represents
CC the cDNA of the wild-type DWf12 locus of the invention
XX
SQ Sequence 1490 BP; 413 A; 340 C; 297 G; 440 T; 0 U; 0 Other;
Query Match 44.8%; Score 733; DB 10; Length 1490;
Best Local Similarity 77.4%; Pred. No. 1e-101;
Matches 889; Conservative 0; Mismatches 260; Indels 0; Gaps 0;
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DB 196 CGCCATGGCTGATGATAGAGAGATGCTGCTGTGTGATGACATGATCAAGTCAC 255
QY 197 CGGTACATATTTCTACTAGCAATTTGGAGGCAAAATGCTGAACCTTAACAGACCATTAG 256

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QY 257 TTACATGCCGAAACGTGTGTTGGAAACAGGATCATTCGGAAATGTATTTCAGGCAAAATG 316
Db 316 TTACATGCCGAGCGAGTTGTTGGTACAGGCTCGTTCGGGATCGTTTTCAGCAAAATG 375
QY 317 CTTGGAACTCGGAATCAGTAGCCATTAAAGAGGTTTTCGAAGATCCCGCTTATATAAAA 376
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QY 497 AGAGACATTTACCGGGTTTGAAGCACTATATAGTTTCAACAGCGGATGCCCTATCTT 556
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QY 917 TCCAACTCGCAAGAAATCCCGTGCATCAACCCAACTACACAGACTTCAGATTTCCCA 976
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QY 1277 ACCCTAGAA 1285
Db 1336 AACTTAAAA 1344

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RESULT 7
AAC47206
ID AAC47206 standard; DNA; 1745 BP.
XX AC AAC47206;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 52951.
XX KW Hybridisation assay; genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway; metabolic pathway;
XX KW promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-00301439.
XX PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
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PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
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XX	ABZ13070 standard; DNA; 1143 BP.	QY	441	TTCTCTCAACGACTAGAGATGAGCTCTTCTCAATCTCGTTATGAGATATGTACCAGAG	500
AC	ABZ13070;	DB	301	TTTTTCGACTACAAAGTAAGAGACGAGCTTTTCTTGAACCTTGTTATGAGATATGTCCTGAG	360
XX	21-JAN-2003 (first entry)	QY	501	ACATTGTACCGGTTTTTGAAGCACTATAGTTTAAACAGCGGATGCTATCTTCTAT	560
XX	Arabidopsis thaliana stress regulated gene SEQ ID NO 875.	DB	361	AGCTTGTATCGAGTTCTGAAACATTTATAGTAGTCAAAACCAAGAAATGCTCTTGTCTAT	420
XX	Arabidopsis thaliana; plant; gene; stress; transgenic; ds.	QY	561	GTCAAACTTTTACACATACCBAATCTTCAGAGGCTTGGCTTATATCCATCTGCTCTGCT	620
XX	Arabidopsis thaliana.	DB	421	GTTAAACTTTTACATGATCAGATCTTCGGGACCTTCTTGTGATCTCTTACTCATCAAGTC	480
XX	WO200216655-A2.	QY	621	GTCTGCCACAGAGATATAAAACCAAAATCTTTTGGTTGATCCCCACACCCATCATGT	680
XX	28-FEB-2002.	DB	481	GTTTGTGCACAGAGATCTAAAGCCTCAAAATCTTCTGGTTGATCCTTCTTACTCATCAAGTC	540
XX	24-AUG-2001; 2001WO-US026685.	QY	681	AAGCTCTGTGATTTTGGAAAGTCAAAAGTACCTGGTGAAGAGGTGAACCAACATATCATAT	740
XX	24-AUG-2000; 2000US-0227866P.	DB	541	AAAACTCTGTGACTTTGGCAGTGCAGAACAGCTCGTTAAAGGTGAAGCCCAACATTTCTTAC	600
XX	22-JUN-2001; 2001US-0300111P.	QY	741	ATCTGCTCTCGGTATTACCGAGCTCCAGAACTCATCTTTGGTGCCACAGAGTATACATCA	800
XX	(SCRI) SCRIPPS RES INST.	DB	601	ATCTGCTCAGATCTTACCGTGCACCGAGCTCATATTTGGTGCCACTGAGTACACACT	660
XX	(SYGN) SYNGENTA PARTICIPATIONS AG.	QY	801	TCCATTGATATATGCTCTGCTGTTGTGTTCTGGCAGAGTACTTCTTGGGAGCGGTTA	860
XX	Harper JF, Kreps J, Wang X, Zhu T;	DB	661	TCTATTGATATCTGGTCTGCTGTTGTGTTCTTGTGAGCTTCTTCTTGTGAGCCATTA	720
XX	WPI; 2002-304127/34.	QY	861	TTCCCGGAGAGAAATTTCTGTGACACAGCTAGTGGAGATCATAAAGTTTCTTGGTACTCCA	920
XX	Identifying a stress condition to which a plant cell has been exposed and	DB	721	TTTCCCGGAGAGAAATGCTGTGGATCAGCTCGTTGAAATTTATAAAAGTTCTTGTGTACCA	780
XX	producing plants with increased tolerance to these abiotic stresses.	QY	921	ACTCGGAGAGAAATCCGGTGCATGAAACCAACTACACAGACTTCCAGATTTCCACAAATC	980
XX	Claim 144; SEQ ID NO 875; 577bp + Sequence Listing; English.	DB	781	ACTCGAGAGAAATCCGTTGTATGATCCACATTTACAGATTTCAAGTTTCCACAGATA	840
XX	The invention relates to identifying a stress condition to which a plant	QY	981	AAAGCCACCCCTTGGCATAAGTTTTTCCAAAGCGGATGCTCCGGAAGCCATTGACCTT	1040
XX	cell has been exposed, comprising: (a) contacting nucleic acid	DB	841	AAAGCCACATCCCTGGCACAAGATCTTCCACAAAAGGATGCCCCACAGAAGCGATTGATTTT	900
XX	representative of expressed polynucleotides in the plant cell with an	QY	1041	GCATCTGGCTCTTCAATACTCACAAGTCTACGTTGACCTGCGCTCGAGGATGTGCG	1100
XX	array or probes representative of the plant cell genome; and (b)	DB	901	GCATCAAGGCTGCTTCAATACTCTCCAACTTAAGATGCACAGCGCTCGAAGGTTGTGCA	960
XX	detecting a profile of expressed polynucleotides in the plant cell	QY	1101	CATCCGTTTTTCAATGAACTCCGTGAGCCAAATGCTGCTTCCAAATGGCCGACCTCTA	1160
XX	characteristic of a stress response. The method is useful in the	DB	961	CATCCGTTTTTGTATGAACTCAGAGAACCAAGCTCGTTTACCAATGGACGCGCTTTC	1020
XX	production of transgenic plants, cells and seeds and in producing plants	QY	1161	CCACCGTTTGTCAACTTCAAAACAAGAGTTGTCTGGGGCTTCCCGGAGCTTATCAACAGG	1220
XX	with increased tolerance to abiotic stress. The present sequence is that	DB	1021	CCGCTCTCTTCAACTTCAAAACAAGAGTAGCTGGATCATCATCTGAACTGGTCAACAAG	1080
XX	of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used	QY	1221	CTAATACACAGAGATGTGAGGCGACAGATGAATGGTGGCTTCCATTTCAAGCTGGACCC	1280
XX	in methods of the invention. Note: The sequence data for this patent is	DB	1081	TTGATTTCCAGACCATATCAAGAGACAATTTGGGTCTAAGCTTCTTGAATCAATCTGAACT	1140
XX	not represented in the printed specification but is based on sequence	QY	1281	TA 1282	
XX	information supplied to Derwent by the European Patent Office	DB	1141	TA 1142	
XX	Sequence 1143 BP; 323 A; 245 C; 247 G; 328 T; 0 U; 0 Other;				
XX	Query Match 44.7%; Score 730.8; DB 6; Length 1143;				
XX	Best Local Similarity 77.5%; Pred. No. 2.2e-101;				
XX	Matches 885; Conservative 0; Mismatches 257; Indels 0; Gaps 0;				
QY	141 ATAGACAAACGACAAAGAAATGTTGCTGCTGTTATAGAGAAATGATGCTGTACCGGT	200			
DB	1 ATGCGCTGATGAAGAGATGCTGCTGCTGTTGATGACATGATCAAGTCACTGGT	60			
QY	201 CACATATTTCTACTACAAATGGAGCAAAAATGGTGAACCTAAACAGACCATAGTTAC	260			
DB	61 CATATTTATTTCCACCAATTCGGTGGCAAAATGGTGAACCAAAACAGACAAATAGTTAC	120			
QY	261 ATGGCCGAACTGTTGTTGGAACAGGATCATTTCCGAATTCATTTCCAGGCAAAATGCTTG	320			
DB	121 ATGGCGGAGCAGTTGTTGTTACAGGCTCGTTCCGGATCGTTTCCAGCAAAATGTTTG	180			
QY	321 GAAATCGAGAAATCAGTAGCCATTAAGAAGTTTTCAGAGATCGCCGTTATAAAAAACCGA	380			
DB	181 GAGACTGGAAGAAACCGTGGCGATAAAGAAGTTTTCAGAGATAGAAGATCAAGAAGCCGA	240			
QY	381 GAGTTGCAATTAATGCGACTAATGACCATCCAAATGCTGTTTCCCTTGAGCAATGTTTC	440			
DB	241 GAACTTCAGTTGATGCGTGTGATGGATCATCCGAATGTGTTTGTGTAAGCAATGCTTC	300			

RESULT 9
ADN73384
ID ADN73384 standard; cDNA; 1143 BP.
XX ADN73384;
XX AC
XX AC
XX AC
XX AC
XX 15-JUL-2004 (first entry)
XX Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1279.
DE gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;
XX growth regulator; animal feed product; thale cress;
KW

cell wall biosynthesis; nitrogen metabolism; carbon metabolism.

Arabidopsis thaliana.

W02004035798-A2.

29-APR-2004.

20-OCT-2003; 2003WO-BP011658.

18-OCT-2002; 2002EP-00079408.

(CROP-) CROPDESIGN NV.

Inze D, De Veylder L, Vlieghe K;

WPI; 2004-348466/32.

P-PSDB; ADN73385.

Altering plant characteristics, useful for producing plants for enzyme or pharmaceutical production comprising modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or more proteins.

Claim 1; SEQ ID NO 1279; 134pp; English.

This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up- or down-regulated in transgenic plants overexpressing the heterodimeric E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, enzymes, therapeutics, pharmaceuticals and animal feed products, where the altered plant characteristics are selected from increased yield or biomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal transduction, storage lipid mobilisation and/or altered photosynthesis, each relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a role in a variety of biological processes such as DNA replication, cell wall biosynthesis, nitrogen and/or carbon metabolism or they function as transcription factors. This polynucleotide sequence is the cress cdna upregulated 1.3 fold or more in plants overexpressing the E2Fa/Dpa transcription factor, given in an exemplification of the invention.

Sequence 1143 BP; 323 A; 245 C; 247 G; 328 T; 0 U; 0 Other;

Query Match 44.7%; Score 730.8; DB 12; Length 1143;

Best Local Similarity 77.5%; Pred. No. 2.2e-101;

Matches 885; Conservative 0; Mismatches 257; Indels 0; Gaps 0;

141 ATAGACAACGACAGGAATGCTGCTGTTATAGAGGAATGATGCTGTACCGGT 200

1 ATGGCTGATGAAGAGAGATGCTGCTGCTGATGATGAGCATGATCAAGTCACTGGT 60

201 CACATAATTTCTACTACAAATGGAGCAAAATGGTGAACCTTAACAGACACCATTAAGTTAC 260

61 CATATTATTTCCACCACATCGGTGGCAAAATGGTGAACCAACAGACACATTAAGTTAC 120

261 ATGGCGGAACGTTGTTGGAGACAGATCATTCGGAAATGTTATTCAGGCAAAATGCTTGG 320

121 ATGGCGGAGCGAGTTGTTGGTACAGGCTGTTTCCGGATCGTTTCCAGCAAAATGTTTG 180

321 GAACTGGAGATCACTAGCCATTAGAGAGTTTTCAGAGTCGCGTTTATTAACCAACCA 380

181 GAGACTGGAGAACCGTGGCGATAAAGAGGTTTTCAGAGTAGAGATACAGAACCA 240

381 GAGTTCGAATTAATGGCACTTAATGGACCATTCAGACCATTCGTTTCCCTTGAAGCATTTGTT 440

241 GAACTTCAGTTGATGCTGATGATCATCCGATGCTGTTGTTTGAAGCATTTGCTTC 300

441 TTCTCTACAAACGACTAGAGATGAGCTCTTCTCAATCTCTGTTATGAGGATGATGACAGAG 500

301	TTTTGCAGTACAAAGTAAAGACGAGCTTTCTTTGAACTTGGTTATGAGTATGTCCCTGAG	360
501	ACATTGTACCGGTTTGAAGCACTATAGTCTCAAAACAGCGGATGCTTCTCTAT	560
361	AGCTTGTATCGAGTCTGAAACATATAGTAGTCAACCAAGAAATGCTCTTGTCTAT	420
561	GTCAAACTTTTACATACCAAACTTTTCAGAGCTTGGCTTATATCATATCTGCTCTGTT	620
421	GTAAACCTTTTACATATCATATCTTCCGGGACTTGTCTTACATTCACAAATGTTGTGGA	480
621	GTCTGCCACAGAGATATAAAACCAAAATCTTTTGGTTGATCCCAACCCATCAGTGT	680
481	GTTCGTACAGAGATCTAAAGCTTCAAAATCTTCTGGTTGATCCCTTCTTACTCATCAAGTC	540
681	AAGCTCTGTGATTTTGGAAAGTCAAAAGTACTGGTGAAGGTGAACCAACCAATATCATAT	740
541	AAATCTGTGACTTTGGCAGTCTCGAAGACAGCTCGTTAAAGGTGAAGCCCAACATTTCTTAC	600
741	ATCTGCTCTCGGTATTAACGAGCTCCAGAACTCATCTTTTGGTGGCCACAGATATACATCA	800
601	ATCTGCTCAGGATTTACCGTGCACCGAGCTCATATTTGGTGGCCACTGAGTACACAACT	660
801	TCCATTGATATATGCTCTGCTGTTGTTCTTGGCAGAGCTACTTCTTGGGAGCGGTTA	860
661	TCATTGATATCTGCTGCTGTTGTTCTTGGTGGCTTCTTCTTGGTCAAGCATTA	720
861	TTCCCGGAGAAATTTCTGTGACAGCTAGTGGAGATCATAAAGTCTTCTTGGTACTCCA	920
721	TTTCCCGGAGAAATGCTGTGATCAGCTCGTGTGAATTAATAAGTCTTCTTGGTACCA	780
921	ACTCGGAAGAAATCCGGTGCATGAACCAAACTACACAGACTTCAGATTCCCAACAAATC	980
781	ACTCGGAAGAAATCCGGTGTATGAATCCACATTACACAGATTTCAGGTTTCCACAGATA	840
981	AAAGCCCACTTGGCATTAAGTTTTCACAGCGGATGCTTCCGGAAGCCATTGACCTT	1040
841	AAAGCAGCATCTCCCTGGCAAGATCTTCCACAAAGGATGCTCCCAAGCGATTGATTT	900
1041	GCATCTCGGCTTCTTCAATCTACCAAGTCTACGTTGACCTGCGCTCGAGGATGTGG	1100
901	GCATCAAGGCTGCTTCAATCTCTCAAGTCTAAGTCAAGCAGCGCTCGAAGCTTGTGCA	960
1101	CATCGGTTTTCATGAATCCGTCGAGCAAAATGCTGCTTTCCAAATGGCCGACCTCTA	1160
961	CATCGGTTTTCATGAATCCGTCGAGCAAAACCAACGCTCGTTTACCAAAATGGACGGCTTC	1020
1161	CCACGCTTGTCAACTTCAACCAAGATGCTTGGGCTTTCACCGGAGCTTATCAACAGG	1220
1021	CGGCTCTCTTCAACTTCAACCAAGATGCTTGGGATCATCACTGAACTGGTCAACAG	1080
1221	CTAATACCAAGAGCATGTGAGGCGACAGATGAATGTTGGCTTTCATTTTCAAGCTGGACCC	1280
1081	TTGATTCAGACCATATCAAGAGCAATTTGGTCTAAGCTTCTTGAATCATCTGGAAT	1140
1281	TA 1282	
1141	TA 1142	

RESULT 10

AAC41916

ID AAC41916 standard; DNA; 1635 BP.

XX AAC41916;

AC AAC41916;

XX 17-OCT-2000 (first entry)

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 33613.

DE Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway; metabolic pathway;

KW promoter; termination sequence; ss.

XX	Arabidopsis thaliana.	PR	29-JUN-1999;	99US-0140991P.
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XX		PR	01-JUL-1999;	99US-0141842P.
PN	EP1033405-A2.	PR	01-JUL-1999;	99US-0142154P.
XX		PR	02-JUL-1999;	99US-0142055P.
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XX		PR	08-JUL-1999;	99US-0142803P.
XX		PR	09-JUL-1999;	99US-0142920P.
PF	25-FEB-2000; 2000EP-00301439.	PR	12-JUL-1999;	99US-0142977P.
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PR	17-JUN-1999;	PR	16-AUG-1999;	99US-0149368P.
PR	18-JUN-1999;	PR	17-AUG-1999;	99US-0149175P.
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PR	18-JUN-1999;	PR	26-AUG-1999;	99US-0150884P.
PR	18-JUN-1999;	PR	26-AUG-1999;	99US-0151065P.
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PR	21-JUN-1999;	PR	30-AUG-1999;	99US-0151303P.
PR	22-JUN-1999;	PR	31-AUG-1999;	99US-0151438P.
PR	23-JUN-1999;	PR	01-SEP-1999;	99US-0151930P.
PR	23-JUN-1999;	PR	07-SEP-1999;	99US-0152363P.
PR	24-JUN-1999;	PR	10-SEP-1999;	99US-0152370P.
PR	28-JUN-1999;			

XX 09-NOV-2001; 2001US-0346096P.
 XX (BADI) BASF PLANT SCI GMBH.
 XX Van Thielien N, Da Costa E SilvaO, Chen R;
 XX WPI; 2003-441522/41.
 XX P-PSDB; ABR42366.
 XX New protein kinase stress-related polypeptide coding nucleic acid, useful
 XX PT for producing transgenic plants with an increased tolerance to an
 XX PT environmental stress, e.g. high salinity, as compared to a wild type
 XX PT variety of the plant.
 XX Claim 1; Page 94-95; 111pp; English.
 XX The present sequence is a full-length cDNA encoding GmpK-1, a novel
 XX CC soybean protein kinase stress-related polypeptide (PKSRP). The cDNA was
 XX CC identified on the basis of homology to Physcomitrella patens PK-3 (see
 XX CC ACC57962) and PK-10 (see ACC57966) sequence. GmpK-1 is an example of
 XX CC PKSRPs of the invention that are important for modulating a plant's
 XX CC response to environmental stress. Over-expression of PKSRP coding nucleic
 XX CC acids in a plant results in the plant's increased tolerance to
 XX CC environmental stress. Transgenic monocot and dicot plants are provided
 XX CC that show increased tolerance to high salinity, drought and low
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ALIGNMENTS

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; APPLICANT: Advanta Seeds B.V.
; TITLE OF INVENTION: Modulation of Storage Organs
; FILE REFERENCE: 026-1
; CURRENT APPLICATION NUMBER: US/09/578.194
; CURRENT FILING DATE: 2000-05-24
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; OTHER INFORMATION: clone lib lambda ZAPII development stage young shoots
; PUBLICATION INFORMATION:
; AUTHORS: Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lecharny, A. and Kreis, M.
; TITLE: Three New cDNAs Related to SGG/GSK-3 (Shaggy/Glycogen Synthase Kinase-3)
; TITLE: from Arabidopsis thaliana (Accession No. 6822139 X94938, x94939 and X99696)
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; JOURNAL: Plant Physiol.
; VOLUME: 113
; ISSUE: 1
; PAGES: 306-306
; DATE: 1997-01-01
; DATABASE ACCESSION NUMBER: genbank/X94938
; DATABASE ENTRY DATE: 1998-02-13
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DB 1197 TTCCGGAACATGTTCCGAGGCAAA 1220

```

RESULT 3

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US-09-854-731-15
; Sequence 15, Application US/09854731
; Patent No. 6794561
; GENERAL INFORMATION:
; APPLICANT: allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases

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; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1349)
; US-09-854-731-15

Query Match      40.8%; Score 667.2; DB 4; Length 1673;
Best Local Similarity 75.3%; Pred. No. 3.3e-141;
Matches 831; Conservative 0; Mismatches 273; Indels 0; Gaps 0;

QY 145 ACAACGACAGGAATGCTCTGCTGTATAGAGGAATGATGCTGTTACCGGTCA 204
DB 117 AGAAGCAGCAGATGGCGGCGCGTATGCGAGGGGAACGACGCCATGACCGGTCA 176
QY 205 TAATTTCTACTACAAATTTGGAGGCAAAATGCTGAACCTAAACAGACCAATTTACATGG 264
DB 177 TCATCTCCACCACTATCGGCGGCAAGAACCGCGAGCCCAAGCAGACGATTAGCTACATGG 236
QY 265 CCGAAACGTGTTGTTGGAAACAGGATCATTTCCGAAATGTTATTCAGGCAAAATGCTTGGAAA 324
DB 237 CCGAGCGGTTGTGGCACTGCTGTTGCTTTGGCATCGTCTTCAGGCTAAATGCTGGAAA 296
QY 325 CTGAGAAATCAAGTACCAATTAAGAAAGTTTTCAGAAATGCGCGTTATATAAACCAGAGAT 384
DB 297 CCGGGAGATGCTGGGCAATTAAGAAAGTACTGACAGACAGACGGTACAAACCGGTGAGC 356
QY 385 TGCAATTAATCGGACTAATGGACCATCCAAATGTTGTTCTTGAAGCATTTGTTCTTCT 444
DB 357 TGCAGCTTATGCGTTCGATGATCCATTCCTCAATGTTGCTCTCCCTCAAGCACTGCTTCTCT 416
QY 445 CTAAACGACTAGAGATGAGCTCTTCTCAATCTCGTTATGGAGTATGTACAGAGACAT 504
DB 417 CAACCAAGTATAGATGAGCTGTTCTGAACTTGTCTATGAGTATGTCCCGGAGACGC 476
QY 505 TGTACCGGTTTGAAGCACTATACAGTTCACAAACAGCGGATGCTTATCTTATGCA 564
DB 477 TATACCGGCTTAAAGCACTACAGTAAATGCAACAGCGGATGCGGCTTATCTATGCA 536
QY 565 AACTTTACATACCAATCTTCAGAGCTTGGCTTATATCCATCTGCTCTCTGCTGCT 624
DB 537 AGCTTTTACATGATCAGCTTTTGAAGGCTAGCTTATGTTTCTATCTGTTCCAGGAGTTT 596
QY 625 GCCACAGAGATATAAACCACAAATCTTTTGGTTGATCCCAACACCCATCAGTGTAAAGC 684
DB 597 GCCACAGGATGTAAACCACAAATGTTTGGTTGATCTCTTAACCCATCAAGTCAAGA 656
QY 685 TCTGTGATTTTGAAGTGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 744
DB 657 TCTGTGATTTTGAAGTGCATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 716
QY 745 GCTCTCGGTATTAACCGAGCTCCAGAACTCATCTTTGGTGGCCACAGAGTATACATCA 804
DB 717 GCTCTCGGTATTAACCGAGCTCCAGAACTCATCTTTGGTGGCCACAGAGTATACATCA 776
QY 805 TTGATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 864
DB 777 TAGACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 836
QY 865 CCGGAGAAATTTCTGTGACAGCTAGTGGAGATCATAAAGTTCTTGGTACTTCCAACTC 924
DB 837 CAGGAGAGACTGCGGTTGATCAGCTAGTGGAGATTAACAAGTTCTTGGTACTTCCAACTC 896
QY 925 GCGAAGAAATCCGGTGCATGAACCAACTACACAGACTTCAGATTCACCAAAATCAAG 984

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Db 897 GTGAGGAAATTCGGTGCATGAACCCCACTATACCGAGTTCAGGTTTCCTCAGATTAAAGG 956
Qy 985 CCACACCTTGGCATTAAGGTTTCCACAGGCGATGCTCCGGAAGCCATGACCTTGCAT 1044
Db 957 CTCATCCTTGGCAACAAGATTTTCCACAGAGAAATGCCCGCTGAAGCTATAGATCTTTGCGCT 1016
Qy 1045 CTCGGCTTCTTCAATACTCAACCAAGTCTAGTTGCACTGGCTCGAGGAGCATGTGCGCATC 1104
Db 1017 CCGCGCTTCTCCAGTATTCACCAAACTACGTTGCGACTGCTCTTGATGATGCGACATT 1076
Qy 1105 CGTTTTTCAATGAACCTCCGTGAGCCAAATGCTCGTCTTCCAAATGCGCCGACCTCTACCCAC 1164
Db 1077 CCTTCTTGATGAGCTACGTGAGCCGAATGCGACGCTTGCAGATGCGCCCATTCCTC 1136
Qy 1165 CGTTGTTCAACTTCAACAAGAGTGTCTCGGGCTTCAACCGGAGCTTATCAACAGGCTAA 1224
Db 1137 CTCGTGTTCACTTCAAAACCTGAACTAGCGAAACGCTCTCCAGAGCTCATCAACAGGCTTG 1196
Qy 1225 TACCAGAGCATGTGAGCGACAGA 1248
Db 1197 TTCGGAACATGTTCAGCGCAAA 1220

RESULT 4

US-09-347-801-9
; Sequence 9, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; EARLIER FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1814
; TYPE: DNA
; ORGANISM: Zea mays
US-09-347-801-9

Query Match 34.1%; Score 557.2; DB 3; Length 1814;
Best Local Similarity 70.9%; Pred. No. 2.4e-116;
Matches 739; Conservative 0; Mismatches 303; Indels 0; Gaps 0;

Qy 141 ATAGACAAACGACGAGGAAATGCTGCTGCTGTTATAGAGGAAATGATGCTGTACCGGT 200
Db 333 ATAGGACGACGAGGACGTTGAAGATATTGTAGTCAATGGCAATGGCGGAGCGCTGGT 392
Qy 201 CACATAATTTCTACTACAATTTGGAGGCAAAATGGTGAACCTTAAACAGACCATTTAGTTAC 260
Db 393 CATATCATAGTGACCACTTTGATGGAGAAATGGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 452
Qy 261 ATGGCGAAGCTGTTGTTGAACAGGATCATTTGGAAATGTTATTCAGGCAAAATGCTTG 320
Db 453 ATGGCTGAGGCGGTGGTGGTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 512
Qy 321 GAACTGAGAAATCAGTAGGACCATTAAGAAGGTTTGAAGATCGCCGTTATATAAAGCCGA 380
Db 513 GAACTGAGGACCGTAGCTATATAAAGGTTCTTCAAGCAAGAGATCAAGATCGT 572
Qy 381 GAGTTGCAATTAATGCGACTAATGAGCAATCCAAATGTTGTTTCTTTGAAGCATTTGTTTC 440
Db 573 GAGCTGCAACCACTGCGAGTGTGACCAACCAAAATGTTGCTCTTAAGCACTGTTTC 632
Qy 441 TTCTCTACAGACTAGAGATGAGCTCTTCTGCTCAATCTGTTATGGAGTATGTACCGAG 500
Db 633 TTCTCAAAGACTGAGAAAGAGGAGCTTTACCTCAATTTGTTGCTTGTGATGTATGACCGAG 692

Qy 501 ACATTGTACCGGTTTTGAAGCACTATATAGTTTCAAAACGAGGATGCCTATCTTCTAT 560
Db 693 ACTGCTCATCGTGTGCATCAAACTTACAACAGATGAACCCAGGCGATGCTTTGATTAT 752
Qy 561 GTCAAACTTTACACATACCAAACTTTCAGAGGCTTTGGCTTATATCATCTACTGCTCTGTT 620
Db 753 GCAAAACCTGTATATGTATCAGATTTGTAGAGCTTTGGCATACATTCACAAACAGCATTTGA 812
Qy 621 GTCTGCCACAGAGATATAAACCACAAATCTTTTGGTTGTATGCCACACACCATCAGTGT 680
Db 813 GTGTGCCACAGGACATTAAGCCGCAAAATCTCCCTGGTTAACTCTATACCATCAGCTA 872
Qy 681 AAGCTCTGTGATTTTGGAGTGCAAAAGTACTGTGGTGAAGGTGAACCAACATATCATAT 740
Db 873 AATTTGTGTGACTTTGGCAGCGGAAAGTTCTGTGTAAGGCGCAACCAACATTTCTTAC 932
Qy 741 ATCTGCTCTCGGTATTTACCGAGCTCCAGAACTCATCTTTTGGTGCCACAGAGTATACATCA 800
Db 933 ATCTGCTCTAGGTACTACAGAGCTCCAGAGCTCATATTTGGTGTCTACTGAATACACAACA 992
Qy 801 TCCATTGATATATGCTGCTGCTGTTGTCTGCGCAGAGCTACTTCTTGGCGAGCCGTTA 860
Db 993 GCAATGATGTTGGGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1052
Qy 861 TTCCCGGAGAGAAATTTCTGTGACGAGCTAGTGGAGATCATAAAGGTTCTTGGTACTCCA 920
Db 1053 TTCCCTGGAGAAAGCGGTGTTGATCAGCTTTGTTGAAATCATCAAGGTTCTGGGCAACCC 1112
Qy 921 ACTCGGAAAGAAATCGGTGCTATGAACCCAACTACAGACTTCAGATTTCCACAAATC 980
Db 1113 ACACGTGAAGAAATTAAGTGCATGAATCCAAATTTATCCGAGTTTAAATTCGCGCAATC 1172
Qy 981 AAAGCCACCTTGGCATTAAGGTTTCCACAAAGCGATGCTCCGAGGAGGATGACCTT 1040
Db 1173 AAAGCTCACCCATGGCATTAAGATTTCCATAAAGGATGCTGCTGAGCGGTAGATCTC 1232
Qy 1041 GCATCTCGGCTTCTTCAATACTACCAAGTCTACGTTGCACTGCGCTCGAGGATGTCG 1100
Db 1233 GTGTCCAGGCTTCTGCACTACTCACCAAACTTCCGCTGCTGCTGCTGCTGCTGCTGCTG 1292
Qy 1101 CATCGGTTTTCAATGAACCTCGGTGAGCCAAATGCTGCTTCCAAATGGCGGACCTCTA 1160
Db 1293 CATCGTTCTTTGATGAACCTTCGGGATCCAAACACCCGCTTACCGAATGGTCTGTTTCT 1352
Qy 1161 CCACGCTGCTTCAACTTCAAC 1182
Db 1353 CCGCTCTCTTCAATTTAAGC 1374

RESULT 5

US-09-854-731-9
; Sequence 9, Application US/09854731
; Patent No. 6794561
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1814
; TYPE: DNA
; ORGANISM: Zea mays
US-09-854-731-9

Query Match 34.1%; Score 557.2; DB 4; Length 1814;
Best Local Similarity 70.9%; Pred. No. 2.4e-116;
Matches 739; Conservative 0; Mismatches 303; Indels 0; Gaps 0;

QY 1048 GCGTCTTCAATACCTACCAAGTCTACGTTGACATGCGCTCGAGGATGTGGCATCGT 1107
Db 1123 GACTACTCAATACCTACCAAGTCTACGTTGACATGCGCTCGAGGATGTGGCATCGT 1182
QY 1108 T---TTTCAATCAATCCGTTGAGCCAAATGCTCGTCTTCCAAATGCGGACCTCTACCA 1164
Db 1193 TTCCTTTGAGCAATCCGNGATCCAAATCTTCGCTTGGCAATGGCGGATCCNTCAA 1242
QY 1165 CGTCTTCAATCCAAACAA 1184
Db 1243 CAATTAATCAAAACCA 1262

RESULT 8

US-09-566-921-24
; Sequence 24, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 24
; LENGTH: 1952
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 234735.15
US-09-566-921-24

Query Match 24.5%; Score 400.8; DB 4; Length 1952;
Best Local Similarity 63.2%; Pred. No. 5.5e-81;
Matches 650; Conservative 0; Mismatches 372; Indels 6; Gaps 2;

QY 217 CAATTGGAGGCAAAATGGTGAACCTTAACAGACATTAGTTACATGCGCGCAATCGTTG 276
Db 204 CCACTCTAGGCGAAGCCGAGCGCTCCCAAGAGTGGCTTACACGACATCAAGTGA 263
QY 277 TTGGAACAGGATCATCTCGAATTTGATTCAGGCAAAATGCTTGAAGCTGAGAAATCAG 336
Db 264 TTGCAATGGCTCATTTGGGTCGTGTACAGGCAAGGCTGCGAGAGACCGAGGACTAG 323
QY 337 TAGCCATTGAAGAGTTTTCAGAGATCCCGTTATATAAACCAGAGTTGCAATTAATGC 396
Db 324 TCGCCATCAAGAAGTTCTCCAGGACAAGAGTTCAAGAACCAGAGCTGCAGATCATGC 383
QY 397 GACTAATGACCATCAATATGTTCTTCTTGAAGCATGTTTCTTC---TACACGA 453
Db 384 GTAAGCTGGACCATGCAATATTTGAGGCTGAGATACCTTTTCTACTCCAGTGGCGAGA 443
QY 454 CTAGAGATGAGCTCTTCCTCAATCTCGTTATGGAGTATGTACAGAGACATTGTACCGGG 513
Db 444 AGAAGAGAGGCTTTACCTAATCTGGTGTGGATATGTGCCGAGACAGTGTACCGGG 503
QY 514 TTTTGAAGCATTACTAGTTCAAAACAGCGGATGCCCTATCTTCTATGTCAAACTTTTACA 573
Db 504 TGGCCCGCCACTTACCAAGGCAAGTTGACCCTATCTCTATGTCAAGGTGTACA 563
QY 574 CATACCAATCTTACAGAGCTTGGCTTATATCACTACTGCTGCTGCTGCGCAGAG 633
Db 564 TGTATCAGCTCTTCCGAGCTTGGCCTACATCCA---CTCCCGAGGCGGTGTGTACACCGC 620
QY 634 ATATAAACCAAAATCTTTTGGTTGATCCCAACACCCATCAGTGTAAAGCTCTGTGATT 693
Db 621 ACATCAAGCCCGAAGCTGTGGTGGACCTTGACATCTGCTGCTCAAGCTCTGCGATT 680

QY 694 TTGGAAGTGCAAAAGTACTGGTGAAGGTGAACCAACATATATATCTCTCGT 753
Db 681 TTGGCAGTGCAGGAGCAGTTGGTCGAGGGGAGCCCAATGTCTCTACATCTCTCGT 740
QY 754 ATTACCGAGCTCCAGAACTCATCTTTGGTGCACAGAGTATACATCATCTTGAATATAT 813
Db 741 ACTACCGGCGCCAGAGCTCATCTTTGGAGCACTGATTAACCTCATCTCGATGTT 800
QY 814 GGTCTGCTGGTTGTCTTGGCAGAGCTACTTTTGGGAGCGCGTTATTTCCCGGAGAAA 873
Db 801 GGTCAAGCTGGCTGTGTACTGGCAGAGCTCTCTTTGGGCGAGCCCATCTTCCCTGGGACA 860
QY 874 ATTCTGTGAGCAGCTAGTGGAGATCAATAAGGTTCTTGGTACTCCAACCTCGGAGAAA 933
Db 861 GTGGGTGGACCACTGGTGGAGATCATCAAGGTGCTGGGAAACCCAAACCCGGGAAACAA 920
QY 934 TCCGCTGATGAACCAAACTACACAGACTTTCAGATTCCCAAAATCAAAAGCCCAACCTT 993
Db 921 TCCGAGAGATGAACCCCAACTACACGGAGTTCAAGTTCCCTCAGATTAAAGCTCACCTT 980
QY 994 GGCATAAGGTTTTCACAAAGCGGATGCTCCGGAAGCATTGACCTTGCATCTCGGCTTC 1053
Db 981 GGACAAAGGTGTTCAAATCTCGAAGCGCGCAGAGGCCATCGCGCTCTGCTTAGCCTGC 1040
QY 1054 TTCAATACTACCAAGTCTAGTTGCACTGGCTCGAGGCAATGCGGATCGGTTTTC 1113
Db 1041 TGGAGTACACCCCATCTCTCAAGGCTCTCCCACTAGAGGCGCTTGGCGACAGCTTCTTTG 1100
QY 1114 ATGAATCTCGTGAGCAAAATGCTGTCTTCCAAATGGCGGAGCTTACACCGTTGTTCA 1173
Db 1101 ATGAATCTCGATGCTTGGGAACCCAGCTGCTTAACACCGGCCACTTCCCTCTCTTCA 1160
QY 1174 ACTTCAAAACAGAGTTGTCTGGGCTTCAACGAGGCTTATCAACAGGCTTAATACAGAGC 1233
Db 1161 ACTTCAGTGTGGTGAACCTCTCCATCAACCGCTCTCTCAAGCCATTTCTCATCCCTCCTC 1220
QY 1234 ATGTGAGG 1241
Db 1221 ACTTGAGG 1228

RESULT 9

US-09-488-856A-3
; Sequence 3, Application US/09488856A
; Patent No. 6316259
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Robert McKay
; APPLICANT: Madeline M. Butler
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 ALPHA EXP
; FILE REFERENCE: RTS-0115
; CURRENT APPLICATION NUMBER: US/09/488,856A
; CURRENT FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
; LENGTH: 2154
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (92)...(1543)
US-09-488-856A-3

Query Match 24.5%; Score 400.8; DB 3; Length 2154;

Best Local Similarity 63.2%; Pred. No. 5.6e-81;
Matches 650; Conservative 0; Mismatches 372; Indels 6; Gaps 2;

QY 217 CAATTGGAGGCAAAATGGTGAACCTTAACAGACATTAGTTATAGTGGCCGAACTGTG 276
Db 405 CCATCTAGGCGCAAGGCCAGCGCTCCCAAGAGTGGCTTACACGACATCAAGTGA 464
QY 277 TTGGAACAGGATCATTCGGAATGTATTTCCAGGCAAAATGTTGGAAACTGGAGAAATCAG 336

Db 465 TTGGCAATGGCTCATTTTGGGGTCGTGTACCGACCGGCTGGCAGAGACCAGGAACTAG 524
Qy 337 TAGCCATTAAGAAGGTTTTCGAAGATCGCGGTTATATAAACCAGAGGTTCGAATTAATGC 396
Db 525 TCGCCATCAAGAAGGTTTCTCCAGGACAAGAGGTTCAAGAACCAGAGAGCTGCGATCATCG 584
Qy 397 GACTAATGACCATCCAAATGTGGTTTCTTGAAGCATTTGTTCTTCTC---TACAACA 453
Db 585 GTAAGCTGGACCACTCAATATTTGAGGCTGAGATACTTTTCTACTCAAGTGGCGA 644
Qy 454 CTAGAGATGAGCTCTTCTCAATCTCGTTATGAGGATGTACAGAGACATTTGTACCGG 513
Db 645 AGAAGACGAGCTTTTACCTAAATCTGTGTGGAATATGTGCCGAGACAGTGTACCGG 704
Qy 514 TTTTGAAGCAGCTATCTAGTTCAACACGAGGATGCTATCTTCTATGTCAAACTTTACA 573
Db 705 TGGCCCGCCACTTCAACAAGGCCAAGTTGACCATCCCTATCTCTATGTCAAGGTGTACA 764
Qy 574 CATACCAAAATCTTCAGAGGCTTGGCTTATATCCATCTGCTCTGCTGTGCTGCACAGAG 633
Db 765 TGTACAGCTCTTCCGAGCTTGGCTTACATCA---CTCCAGGCGGTGTACCGG 821
Qy 634 ATATAAAACCAAAAATCTTTTGGTTGATCCCCACACCCCATCAGTGTAAAGCTCTGTGAT 693
Db 822 ACATCAAGCCCCAGAACCTTGCTGGTGACCTTGACACTGTGTCTCAAGCTCTGGGAT 881
Qy 694 TTGGAAGTGAAGAAGTACTGTTGAAGGTGAACCAAAATATCATATATCTGCTCTCGGT 753
Db 882 TTGGCAGTGCAAAGCAGTTGGTCCGAGGGAGGCCAAATGTCTCTACATCTGTCTCGCT 941
Qy 754 ATTACCGAGCTCCAGAACCTCATCTTTGTTGCGACAGAGTATACATCATCTTGTATATAT 813
Db 942 ACTACCGGGCCAGAGCTCATCTTTGGAGCCACTGATTACACCTCATCATCGATGTTT 1001
Qy 814 GGTCTGCTGTGTGTCTGGCAGAGCTACTTCTGGGCGAGCGGTTATTTCCCGGGAGAAA 873
Db 1002 GGTCACTGGCTGTGTACTGGCAGAGCTCTCTTTGGGCCAGGCCATCTTCCCTGGGACA 1061
Qy 874 ATTCTGTGACAGCTAGTGGAGATCATTAAGGTTCTTGGTACTCCAACTCCGGAAGAAA 933
Db 1062 GTGGGGTGGACCAAGCTGGTGGAGATCATCAAGGTGCTGGGAAACACCAACCCGGGAA 1121
Qy 934 TCCGCTGCAATGAACCAACTACAGACTTTCAGATTCCCAAAATCAAAAGCCACCCCTT 993
Db 1122 TCCGAGAGATGAACCCCACTACACGAGTTTCAAGTTTCCCTCAGATTAAGCTCACCCCT 1181
Qy 994 GGCATAAGGTTTTCACAAGCGGATGCTCCGGAAGCCATTGACCTTGCATCTCGGCTTC 1053
Db 1182 GGACAAAGGTTTCAAAATCTCGAAGCGCGCCAGAGGCCATCGCGCTCTGCTTAGCCTGC 1241
Qy 1054 TTCAATCTACCAAGTCTAGTTGCACTGCGCTCGAGGATGTGCGCATCGGTTTTCAT 1113
Db 1242 TGGAGTACACCCCATCTCAAGGCTCTCCCACTAGAGGCTCTGGCGCAGCTTCTTTTG 1301
Qy 1114 ATCAACTCCGTGAGCAAAATGCTCTTCCAAATGGCGACCTCTACCAACCGTTGTTCAT 1173
Db 1302 ATGAAGTTCGATGCTGGGAACCCAGTGTGCTTAACACGCCCACTTCCCTCTCTTCA 1361
Qy 1174 ACTTTCAAAACAAGATTTGTCTGGGGCTTTCACCGAGCTTTATCAACAGGCTTAATCAAGAG 1233
Db 1362 ACTTCAGTGTGTGAACCTCTCCATCCAAACCGTCTCTCAAGGCCATTTCTCATCCCTCCTC 1421
Qy 1234 ATGTGAGG 1241
Db 1422 ACTTGAGG 1429

RESULT 10
US-09-489-765A-3
; Sequence 3, Application US/09489765A
; Patent No. 6323029
; GENERAL INFORMATION:

; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRESSION
; FILE REFERENCE: RTS-0124
; CURRENT APPLICATION NUMBER: US/09/489,765A
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 85
; SEQ ID NO 3
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (40)...(1302)
US-09-489-765A-3

Query Match 24.2%; Score 395.6; DB 3; Length 1389;
Best Local Similarity 65.6%; Pred. No. 7,3e-80;
Matches 610; Conservative 0; Mismatches 314; Indels 6; Gaps 2;

Qy 253 TTAGTTACATGCGCCGAAAGTGTGTTGGAAACAGGATCATTCGGAATTTGATTTCCAGGCAA 312
Db 200 TCAGCTATACAGACACTAAAGTGAATTGGAATGGATCATTTGGTGTGTATATCAAGCCA 259
Qy 313 AATGCTTGGAAACTGGAGAAATCAGTAGCCATTAAGAAGGTTTTGCAAGATCGCGTTATA 372
Db 260 AACTTTGTGATTTCAGAGAACTGGTCCCATCAAGAAAGTATTGCAAGCAAGAGATTTA 319
Qy 373 AAAACCGAGAGTTTCAAAATTAATTCGCACTAAATGGACCATCCAAATGTGGTTTCTTTGAAGC 432
Db 320 AGAATCGAGAGCTCCAGATCATGAGAAAGTAGATCACTGTAAACATAGTCCGATTCGGTT 379
Qy 433 ATGTTTCTTCTC---TACAACGACTAGAGATGAGCTCTTCTCTCAATCTCTGTTATGAGT 489
Db 380 ATTCTCTTCTACCTCCAGTGGTGAGAAAGATGAGGTCTATCTTAATCTGTGTGCTGACT 439
Qy 490 ATGTACACGAGACATGTACCGGTTTTGAAGCACTATATAGTTTCAAAACCGAGCGATGC 549
Db 440 ATGTTCCGGAACAGTATACAGAGTTGCCAGACACTATAGTCCAGCCAAACAGACGCTCC 499
Qy 550 CTATCTTCTATGTCAAACTTTACACATACCAATCTTCAGAGGCTTTGGCTTATATCCATA 609
Db 500 CTGTGATTTATGTCAAGTTGTATATGATCAGCTGTTCGGAAGTTTGTAGCTATATCCA-- 557
Qy 610 CTGCTCTCGGTGTGCGCACAGAGATATAAAACCAAAAATCTTTTGGTTGATCCCCACA 669
Db 558 -TTCCCTTTGGAATCTGCCATCGGGATATTAAACCCGAGAACTCTTTGTTGGATTCCTGATA 616
Qy 670 CCCATCAGTGTAGCTCTGTGATTTTGGAAAGTGCAAAAGTACTGTGTGAAAGGTGAACCAA 729
Db 617 CTGCTGTATTAAACTCTGTGACTTTTGGAAAGTGCAAAAGCAGCTGTGTCGAGGAGAACCCA 676
Qy 730 ACATATCATATATCTGCTCTCGGTATTCAGGAGCTCCAGAGCTCATCTTTGTTGGCCACAG 789
Db 677 ATGTTTTCGTATATCTGTTCTCGTACTATAGGACACACAGAGTTGATCTTTTGGAGCCACTG 736
Qy 790 AGTATACATCATCCATTGATATATGCTCTGCTGGTTGTGTTCTTGGCAGAGACTACTTCTTG 849
Db 737 ATTATACCTCTAGTATAGATGTATGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 796
Qy 850 GGCAGCGGTTATTTCCCGGAGAGAAATTTCTGTGACCGAGCTAGTGGAGATCATATAAGGTTTC 909
Db 797 GACAAACAATTTTCCAGGGATAGTGGTGTGATCAGTTGTGAGAAATATCAAGGTCC 856
Qy 910 TTGGTACTCCAACTCGCGAAGAAATCCGGTGTGATGAACCCAAACTACACAGACTTCAGAT 969
Db 857 TGGGAATCCCAACAGGAGGCAAAATCAGAGAAATGAACCCAAACTACACAGAAATTTAAAT 916
Qy 970 TCCCAAAATCAAGCCCACTCTTGCATAGAGTTTTCACAGCGGATGCTCTCCCGAG 1029
Db 917 TCCCTCAAAATTAAGGCACATCTCTTGGACTTAAGGTCTTTCGAGCCCGGAGG 976

QY 1030 CCATTGACCTTGCATCTCGGCTTCTTCAATCTACCAAGTCTACGTTGCACCTGGCTCG 1089
DB 977 CAATTGCACTGTGTAGCCGTCTGCTGGAGTATACACCAACTGCCGCACTAAACACCACTGG 1036
QY 1090 AGGCATGTCGGATCGGTTTTCATGAAGTCTCGTGAGCCAAATGCTGCTCTTCCAAATG 1149
DB 1037 AGCTTGTGCACATTCATTTTTGTGATGAATAGGGACCCAAATGTCAAAATCCAAATG 1096
QY 1150 GCCGACCTCTACCACTGGTTTCAACTCA 1179
DB 1097 GCGGAGACACCTGCACTCTTCAACTCA 1126

RESULT 11

US-09-016-434-1414
; Sequence 1414, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1414:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1389 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: 9529236
; US-09-016-434-1414

Query Match 24.2%; Score 395.6; DB 4; Length 1389;
Best Local Similarity 65.6%; Pred. No. 7.3e-80;
Matches 610; Conservative 0; Mismatches 314; Indels 6; Gaps 2;
QY 253 TTAGTTACATGCCGCACTGTGTGTGGAACAGGATCAATTCGGAATGTATTCCAGGCAA 312
DB 200 TCAGCTATACAGACACTAAAGTGAATGGAATGGATCATTTGGTGTGTATATCAAGCCA 259
QY 313 AATGCTTGGAACTGGAGATCAGTAGCCATTAAGAGGTTTGGCAAGTCCGCTTATA 372
DB 260 AACTTTGTGATTCAGGAGAACTGGTCCGCAATCAAGAAAGTATTTCAGGACAGAGATTTA 319

QY 373 AAAACCGAGAGTTGCAATTAATGCGACTAAATGGACCATCCAAATGTGGTTTCTTCTGAAGC 432
DB 320 AGAATCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAAACATAGTCCGATGGCTT 379
QY 433 ATTGTTTCTTCTC---TACAACGACTAGAGATGAGCTCTTCTCTCAATCTCGTTATGGAGT 489
DB 380 ATTTCTTCTTACTCCAGTGGTGAGAAAGAGTGGGTCTATCTTAACTCTGGTGGCTGAGCT 439
QY 490 ATGTACACAGACATTTGTACCGGTTTGAAGCACTATATAGTTCAAAACACGCGATGC 549
DB 440 ATGTTCCGGAACAGTATACAGAGTTGCCAGACACTATAGTCGAGCCAAACAGACGCTCC 499
QY 550 CTATCTTCTATGTCAAACTTTACACATACCAAACTTTCAGAGGCTTGGCTTATATCCATA 609
DB 500 CTGTGATTTATGTCAAAGTTGTATATGTATGATGCTGTCGAAAGTTTAGCTATATCCA-- 557
QY 610 CTGCTCTGCTGCTGCCACAGAGATATAAACCACCAAAATCTTTTGGTGTGATCCCCACA 669
DB 558 -TTCTTTTGAATCTGCCATCGGATATTTAAACCGCAGAACCTCTTGTGGATCCTGATA 616
QY 670 CCCATCAGTGTAAAGCTCTGTGATTTTGAAGTGCAAAAGTACTGTGAAAGGTGAACCAA 729
DB 617 CTGCTGTATTAAGACTCTGTGACTTTTGGAGTGCAGACGCTGTCGAGAGAGAACCA 676
QY 730 ACATATCATATATCTGCTCTCGGTATTAACGAGCTCCAGAACTCATCTTTTGGTGCACAG 789
DB 677 ATGTTTCGTATATCTGTTCTCGGTACTATAGGGCACAGAGTTGATCTTTGGAGCCACTG 736
QY 790 AGTATACATCATCCATTCATATATGTTCTGCTGGTGTGTCTGCGCAGAGCTACTTCTTG 849
DB 737 ATTATACCTTAGTATAGATGTATGCTGCTGGCTGTGTGTGCTGAGCTGTACTAG 796
QY 850 GCGAGCCGTTATTCGCGGAGAGAAATTCGTGGACAGCTAGTGGAGATCATAAAGGTTTC 909
DB 797 GACAAACCAATATTTCCAGGGGATAGTGTGTGGATCAGTTGTTAGAAATATCAAGTCC 856
QY 910 TTGTTACTCCAACTCGCGAAGAAATCCGTTGCATGAACCCCAAACTTACAGACTTTCAGAT 969
DB 857 TGGGAACCTCCAAAGGAGCAAAATCAGAGAAATGAACCCAACTTACAGAAATTTAAAT 916
QY 970 TCCCAAAATCAAAGCCCACTTGGCATAGTTTTCACAGCGGATGCTCTCGGAAG 1029
DB 917 TCCCTCAAATTAAGGCACATCTTTGGACTTCTCCGACCCCGGAACTCCACCGGAGG 976
QY 1030 CCATTGACCTTGCATCTCGGCTTCTTCAATCTACCAAGTCTAGCTTGCCTGCTCG 1089
DB 977 CAATTGCACTGTGTAGCCGTCTGCTGGAGTATACACCAACTGCCGCACTAACCACTGG 1036
QY 1090 AGGCATGTCGCATCCGTTTTCATGAAGTCCGTTGAGCCAAATGCTGCTTCCAAATG 1149
DB 1037 AAGCTTGTGCACATTCATTTTGTATGAATTAAGGGACCCAAATGTCAAAACATCCAAATG 1096
QY 1150 GCCGACCTCTACCACTGGTTTCAACTTCA 1179
DB 1097 GCGGAGACACACCTGCACTCTTCAACTTCA 1126

RESULT 12

US-08-602-264A-1
; Sequence 1, Application US/08602364A
; Patent No. 5837853
; GENERAL INFORMATION:
; APPLICANT: Akihiko TAKASHIMA et al.

; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.

ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,264A
FILING DATE: February 20, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2088 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORGANISM: human being
US-08-602-264A-1

Query Match 24.1%; Score 394; DB 2; Length 2088;
Best Local Similarity 65.5%; Pred. No. 1.9e-79;
Matches 609; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

QY 253 TTATGTTACATGGCGGAACGTGTTGGTGAACAGGATCATTCGGAATGTTATCCAGGCAA 312
DB 776 TCAGCTATACAGACTAACTCAATGGAAATGATCATTTGGTGGTATATCAAGCCA 835
QY 313 AATGCTTGGAAATCGAGAAATCAGTAGCCATTAAGAAAGTTTTCGAAGATCGCGGTATA 372
DB 836 AACTTTGTGATTCCAGGAGACTGTCGCCATCAAGAAAGTATTTCGAGGCAAGAGATTTA 895
QY 373 AAACCGAGATGGCAATTAATCGCATATGAGCAATCAAAATGTTGTTTCCTTGAAGC 432
DB 896 AGAATCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAACATAGTCCGATTGCGTT 955
QY 433 ATTGTTCTTCTC--TACAAAGACTAGAGATGAGTCTTCTCAATCTCGTTATGAGT 489
DB 956 ATTCTTCTACTCCAGTGGTGAAGAAAGATGAGGTCTATCTTAATCTGGTCTGAGT 1015
QY 490 ATGTACAGAGACATTTGATCCGGTGTGAAAGCACTATACCTAGTCAAAACCGAGGATGC 549
DB 1016 ATGTTCCGGAAACAGTATACAGAGTTGCCAGACACTATAGTCAGCAACACAGACGCTCC 1075
QY 550 CTATCTTCTATGTCAAACTTTACACATACCAAAATCTTCAGAGGCTTGGCTTATATCCATA 609
DB 1076 CTGTGATTATGTCAAGTTGTATATGTATCAGCTGTTCCGAAGTTAGCCATATATCCA-- 1133
QY 610 CTGCTCCTGTGCTGCCACAGAGATATAAACCACAAATCTTTTGGTTGATCCCA 669
DB 1134 -TTCTTTTGGAAATCGCATCGGGGATATTAACCGCAGAAACCTCTTGTGGATCCTGATA 1192
QY 670 CCCATCAGTGAAGCTCTGTGATTTTGGAAAGTCAAAAGTACTGTCGAAAGGTGAACCAA 729
DB 1193 CTGCTGTATTAACACTGTGACTTTGGAGTGCMAAGCAGCTGTCGAGGAGAGACCCA 1252
QY 730 ACATATCATATATCTGCTCTCGGTATTAACGAGTCCAGAACTCATCTTTGGTGGCCACAG 789
DB 1253 ATGTTTCGTATATCTGTTCTCGTCTACTATATAGGCAACAGAGTTGATCTTTGGAGCCACTG 1312

QY 790 AGTATACATCATCCATTGATATATATGCTGCTGGTGTGTTCTTGGCAGAGCTACTTCTTG 849
DB 1313 ATTATACCTCTAGTATAGATGATGCTGCTGGCTGTGTTGGCTGAGCTGTACTAG 1372
QY 850 GGCAGCCGTTATTCGGGAGAAATTCCTGTGGACAGCTAGTGGAGATCATAAAGGTTTC 909
DB 1373 GACAAACCAATATTCAGGGGATAGTGGTGTGGATCAGTTGTAGAAAATAATCAAGGTCC 1432
QY 910 TTGGTACTCCAACTCGCGAAGAAATCCGGTGCATGAACCCAACTACACAGACTTCCAGAT 969
DB 1433 TGGGAACCTCAACAAAGGGAGCAATCAGAGAAATGAACCCAACTACACAGAAATTTAAAT 1492
QY 970 TCCCAAAATCAAAGCCACCCCTTGGCATAAAGTTTTTCCAAGCGGATGCTCCGGAAG 1029
DB 1493 TCCCTCAATTAAGGACATCTCTGGACTAAGTCTTCCGACCCCGAAGCTCCACCGGAGS 1552
QY 1030 CAATTGACCTTGCACTCTCGGCTTCTTCAATATCTACCAAGTCTAGTTCGACTGCGCTCG 1089
DB 1553 CAATTGCACTGTAGCCGCTCTGCTGGAGTATACACCAACTGCCGACTAACACCACTGG 1612
QY 1090 AGGCATGTGGCATCGGTTTTTCAATGAACCTCGGTGAGCCAAATGCTCGTCTTCCAAATG 1149
DB 1613 AAGCTTGTGCACATCATTTTGTGATGAATTAACGGAGCCAAATGTCAAACTACCAATG 1672
QY 1150 GCCGACCTCTACCAACCGCTTGTTCAACTTCA 1179
DB 1673 GCGGAGACACACTGCACTTCAACTTCA 1702

RESULT 13

US-08-461-018A-1
Sequence 1, Application US/08461018A
Patent No. 6071694
GENERAL INFORMATION:
APPLICANT: Akihiko TAKASHIMA et al.
TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: WENDERTH, LIND & POWACK
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,018A
FILING DATE: June 5, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/204,091
FILING DATE: March 2, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2088 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE:

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US-08-461-018A-1
ORGANISM: human being
Query Match      24.1%; Score 394; DB 3; Length 2088;
Best Local Similarity 65.5%; Pred. No. 1.9e-79;
Matches 609; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

QY 253 TTAGTTACATGCGCCGAACTGTTGTTGGAACAGGATCATTCGGAATTTGTTATCCAGGCAA 312
DB 776 TCAGCTATACAGACACTAAACTCATTTGGAATGGATCATTTGGTGTGTATATCAAGCCA 835
QY 313 AATGCTTGGAACTCGAGAACATGAGCCATTAAGAAAGTTTGAAGATCCCGGTTATA 372
DB 836 AACTTTGTGATTCAGGAACTGTTGCGCCATCAAGAAAGTATTGCGAGCAAGAGATTTA 895
QY 373 AAAACCGAGAGTGCATTAATTAATGCACTTAATGGAACCATCCAAATGTTGGTTTCCTTGAAC 432
DB 896 AGAATCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAACATAGTCCGATTTGGTT 955
QY 433 ATTGTTCTTCTC---TACAAGACTAGAGATGAGCTCTTCTCAATCTCGTTATGGAGT 489
DB 956 ATTCTTCTACTCCAGTGGTGAAGAAAGATGAGTCTATCTTAATCTGGTGTGGACT 1015
QY 490 ATGTACACAGACATTTGATCCGGGTTTGAAGACTATCTAGTTTCAACACCGGATGC 549
DB 1016 ATGTTCCGAAACAGTATACAGAGTTGCGAGACACTATAGTCGAGCCAAACAGACGCTCC 1075
QY 550 CTATCTTCTATGTCAAACTTTTACACATACCAAACTTTTTCAGAGGCTTGGCTTATATCCATA 609
DB 1076 CTGTGATTTATGTCAAGTTGTATATCTATCACTGTTCCGAGTTTAGCTATATCCA-- 1133
QY 610 CTGCTCCTGTTGTCGCCACAGAGATATAAAACCAAAATCTTTTGGTTGATCCCAACA 669
DB 1134 -TTCCTTTGGAATCTGCCATCGGATATTAACCCGAGAACCTCTTTTGGATCCTGATA 1192
QY 670 CCCATCAGTGAAGCTCTGTGATTTTGGAGTGCAGAAAGTACTGTTGGAAGTGAACCA 729
DB 1193 CTGCTGTATTAATACTCTGTGACTTTGGAAGTGCAGAACGCTGTTGCGAGGAGAACCCA 1252
QY 730 ACATATCATATATCTGCTCTCGGTATTACCGAGCTCCAGAACTCATCTTTTGGTGCACAG 789
DB 1253 ATGTTTCTGATATCTGTTCTCGTACTATAGGACACAGAGTTGATCTTTGAGCCACTG 1312
QY 790 AGTATACATCATCCATTTGATATATGTTCTGCTGTTGTTGTTCTTGGCAGAGTACTTCTTG 849
DB 1313 ATTATACCTCTAGTATAGATGATGTTCTGCTGCTGTTGTTGCTGAGCTGTTACTAG 1372
QY 850 GCGACCGTTATTCGGGAGAAATTTCTGTCGACCGCTAGTGGAGATCATATAAGGTTTC 909
DB 1373 GACAAACCAATATTTCCAGGGGATGTTGTTGCTGATCAGTTGTTGAAAATAATCAAGGTCC 1432
QY 910 TTGGTACTCCTCACTCGCGAAGAAATCCGTTGATGAACCCAACTTACACAGACTTTCAGAT 969
DB 1433 TGGGAATCTCAACAGGAGGAAATCAGAGAATGAACCCAACTTACACAGAAATTAAT 1492
QY 970 TCCCAAAATCAAGCCCACTTGGCATTAAGTTTTCACAAAGCGGATGCTCCCGGAAG 1029
DB 1493 TCCCTCAAATTAAGGCACATCTTGGACTTAAGTTCTTCCGACCCCGAATCTCCACCGGAG 1552
QY 1030 CAATTGACCTTGATCTCGGCTTCTTCAATCTACCAAGTCTAGTTGCACTGCGCTCG 1089
DB 1553 CAATTGCACTGTTAGCGCTGCTGCTGGAGTATACACCAACTGCTCCGACCTTAACACCACTGG 1612
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DB 1613 AGCTTGTGCAATTCATTTTGTGATTAATACGGAGCCAAATGTCAAACTTACCAATG 1672
QY 1150 GCCGACCTCTACACCGTTGTTCAACTTCA 1179
DB 1673 GCGGAGACACACTGCACTCTTCAACTTCA 1702

US-09-216-958-1
Sequence 1, Application US/09216958
Patent No. 6248559
GENERAL INFORMATION:
APPLICANT: AKIHIKO TAKASHIMA et al.
TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESS: WENDEROTH, LIND & PONACK
CITY: Washington
COUNTRY: D.C.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch,
MEDIUM TYPE: 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/216,958
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/461,018
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2088 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to genomic RNA
ORIGINAL SOURCE:
ORGANISM: human being
US-09-216-958-1
Query Match      24.1%; Score 394; DB 3; Length 2088;
Best Local Similarity 65.5%; Pred. No. 1.9e-79;
Matches 609; Conservative 0; Mismatches 315; Indels 6; Gaps 2;

QY 253 TTAGTTACATGCGCCGAACTGTTGTTGGAACAGGATCATTCGGAATTTGTTATCCAGGCAA 312
DB 776 TCAGCTATACAGACACTAAACTCATTTGGAATGGATCATTTGGTGTGTATATCAAGCCA 835
QY 313 AATGCTTGGAACTCGAGAACATGAGCCATTAAGAAAGTTTGAAGATCCCGGTTATA 372
DB 836 AACTTTGTGATTCAGGAACTGTTGCGCCATCAAGAAAGTATTGCGAGCAAGAGATTTA 895
QY 373 AAAACCGAGAGTGCATTAATTAATGCACTTAATGGAACCATCCAAATGTTGGTTTCCTTGAAC 432
DB 896 AGAATCGAGAGCTCCAGATCATGAGAAAGCTAGATCACTGTAACATAGTCCGATTTGGTT 955
QY 433 ATTGTTCTTCTC---TACAACGACTAGAGATGAGCTCTTCTCAATCTCGTTATGGAGT 489
DB 956 ATTCTTCTACTCCAGTGGTGAAGAAAGATGAGTCTATCTTAATCTGGTGTGGACT 1015
QY 490 ATGTACACAGACATTTGATCCGGGTTTGAAGACTATCTAGTTTCAACACCGGATGC 549
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QY 550 CTATCTTCTATGTCAAACTTTTACACATACCAAACTTTTTCAGAGGCTTGGCTTATATCCATA 609
DB 1076 CTGTGATTTATGTCAAGTTGTATATCTATCACTGTTCCGAGTTTAGCTATATCCA-- 1133
QY 610 CTGCTCCTGTTGTCGCCACAGAGATATAAAACCAAAATCTTTTGGTTGATCCCAACA 669
DB 1134 -TTCCTTTGGAATCTGCCATCGGATATTAACCCGAGAACCTCTTTTGGATCCTGATA 1192
QY 670 CCCATCAGTGAAGCTCTGTGATTTTGGAGTGCAGAAAGTACTGTTGGAAGTGAACCA 729
DB 1193 CTGCTGTATTAATACTCTGTGACTTTGGAAGTGCAGAACGCTGTTGCGAGGAGAACCCA 1252
QY 730 ACATATCATATATCTGCTCTCGGTATTACCGAGCTCCAGAACTCATCTTTTGGTGCACAG 789
DB 1253 ATGTTTCTGATATCTGTTCTCGTACTATAGGACACAGAGTTGATCTTTGAGCCACTG 1312
QY 790 AGTATACATCATCCATTTGATATATGTTCTGCTGTTGTTGTTCTTGGCAGAGTACTTCTTG 849
DB 1313 ATTATACCTCTAGTATAGATGATGTTCTGCTGCTGTTGTTGCTGAGCTGTTACTAG 1372
QY 850 GCGACCGTTATTCGGGAGAAATTTCTGTCGACCGCTAGTGGAGATCATATAAGGTTTC 909
DB 1373 GACAAACCAATATTTCCAGGGGATGTTGTTGCTGATCAGTTGTTGAAAATAATCAAGGTCC 1432
QY 910 TTGGTACTCCTCACTCGCGAAGAAATCCGTTGATGAACCCAACTTACACAGACTTTCAGAT 969
DB 1433 TGGGAATCTCAACAGGAGGAAATCAGAGAATGAACCCAACTTACACAGAAATTAAT 1492
QY 970 TCCCAAAATCAAGCCCACTTGGCATTAAGTTTTCACAAAGCGGATGCTCCCGGAAG 1029
DB 1493 TCCCTCAAATTAAGGCACATCTTGGACTTAAGTTCTTCCGACCCCGAATCTCCACCGGAG 1552
QY 1030 CAATTGACCTTGATCTCGGCTTCTTCAATCTACCAAGTCTAGTTGCACTGCGCTCG 1089
DB 1553 CAATTGCACTGTTAGCGCTGCTGCTGGAGTATACACCAACTGCTCCGACCTTAACACCACTGG 1612
QY 1090 AGGCAATGTCGATCCGTTTTCATGAACCTCGGTGAGCAAAATGCTGCTTCCAAATG 1149
DB 1613 AGCTTGTGCAATTCATTTTGTGATTAATACGGAGCCAAATGTCAAACTTACCAATG 1672
QY 1150 GCCGACCTCTACACCGTTGTTCAACTTCA 1179
DB 1673 GCGGAGACACACTGCACTCTTCAACTTCA 1702

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QY 610 CTGCTCTGGTGTCTGCCACAGAGATATAAAACCAACCAAAATCTTTGGTTGATCCCA 669
Db 1134 -TTCTTTGGAATCTGCCATCGGATATTAAACCGCAGAACCTCTTGTGGATCTGTAT 1192
QY 670 CCCATCAGTGTAAAGTCTGTGATTTTGGAAAGTCAAAAGTACTGTGTGAAGGTGAACCAA 729
Db 1193 CTGCTGTATTAACAACTCTGTGACTTTTGGAAAGTCAAAAGCAGCTGTGCCAGGAGAACCA 1252
QY 730 ACATATCATATATCTCTCTCGGTATACCGAGCTCCAGAACTCATCTTTGGTGCACAG 789
Db 1253 ATGTTTCTGATATCTCTCTCGGTATACCGAGCTCCAGAACTCATCTTTGGTGCACAG 1312
QY 790 AGTATACATCATCAATTTGATATATGCTCTGTGTTGTTCTTGGCAGAGCTACTTCTTG 849
Db 1313 ATTATACCTCTAGTATAGATATGTTCTGTGCTGTGTTGCTGTGCTGTGCTGTGCTGT 1372
QY 850 GGCAGCCGTTATTTCCGGGAGAGAAATTTCTGTGACAGCTAGTGTGAGATCATATAAGTTTC 909
Db 1373 GACAAACCAATATTTCCAGGGGATAGTGTGTGATCAGTTGGTAGAAATAATCAAGGTCC 1432
QY 910 TTGGTACTCAACTCCGGAAGAAATCCGGTGCATGAAACCCAACTACACAGACTTCAGAT 969
Db 1433 TGGGAATCTCAACAGGGAGCAAAATCAGAGAAATGAACCCAACTACACAGAAATTTAAAT 1492
QY 970 TCCCAAAATCAAAGCCCACTTGGCATAAGGTTTTCACAAAGCGGATGCTCCGGAAG 1029
Db 1493 TCCTCAATTAAGGCACATCTTGGACTAAGTCTTCCGACCCCACTCCACCGGAG 1552
QY 1030 CCATGACCTTGCATCTCGGCTTCTTCAATATCTACCAAGTCTACGTTGCACTCGCTCG 1089
Db 1553 CAATTGCACTGTAGCGCTCTCTGGAGTATACACCAACTGCGCCGACTAACACCACTGG 1612
QY 1090 AGCATGTGGCATCGTTTTCATGAAGTCTCGTGAGCGCAATGCTCTTCCAAATG 1149
Db 1613 AGCTTGTGCACATTCATTTTGTATGAAATACGGGACCCAAATGCAAACTACCAATG 1672
QY 1150 GCGGACCTCTACCACTGTTTCAACTTCA 1179
Db 1673 GCGGACACACCTGCACTTCAACTTCA 1702

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RESULT 15
US-08-602-264A-2
; Sequence 2, Application US/08602264A
; Patent No. 5837853
; GENERAL INFORMATION:
; APPLICANT: Akihiko TAKASHIMA et al.
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF ARZHEIMER'S DISEASE
; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,264A
; FILING DATE: February 20, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/204,091
; FILING DATE: March 2, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.

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; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1972 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to genomic RNA
; ORIGINAL SOURCE:
; ORGANISM: rat
; US-08-602-264A-2

Query Match 23.8%; Score 390; DB 2; Length 1972;
Best Local Similarity 64.2%; Pred. No. 1.5e-78;
Matches 620; Conservative 0; Mismatches 340; Indels 6; Gaps 2;

QY 217 CAATTGGAGGCAAAATCGTGAACCTTAAACAGACCATTTAGTTACATGGCGGAAACGTTG 276
Db 264 CAACTCTTGACAGGGTCTTGACAGGCCACAGGAAGTCAGTTACACAGACACTTAAAGTCA 323
QY 277 TTGGAAACAGGATCATTTCCGGAATTTGTTATCCAGGCAAAATGCTTGGAAAACCTGGAGAAATCAG 336
Db 324 TTGGAAATGGGTCTATTTGGTGTGTATATCAAGCCAAACTTTGTGACTCAGGGAATCG 383
QY 337 TAGCCATTAAAGAGTTTTCGCAAGATTCGCGGTTATAAAACCGAGAGTTGCAATTAATGC 396
Db 384 TGGCCATCAAGAAAGTTCTTCAGGACAGCGATTTAAGAACCGAGAGCTCCAGATCATGA 443
QY 397 GACTAATGACACATCCAAATGTTTCTTGAAGCAATGTTTCTTCTC---TACAAACA 453
Db 444 GAAAGTAGATCACTGTGTAAACATAGTCCGATTCGGGTATTTCTTCTACTCGAGTGGCGAGA 503
QY 454 CTAGAGATGAGCTTCTCTCAATCTGTTATGGAGTATGTACAGAGACATTTGTACCGGG 513
Db 504 AGAAGATGAGGTCTACCTTTAACTGCTGCTGATATGTTCCGGAACAGTGTACAGAG 563
QY 514 TTTTGAAGCACTATATAGTTCAAAACCGAGGATGCTATCTTTCTATGTCAAACTTTTACA 573
Db 564 TCGCCAGACATATATAGTCGAGGCAAGCAGACACTCCCTGTGATCTATGTCAAGTTGTATA 623
QY 574 CATACCAATCTTCAGAGCTTGGCTTATATCCATATCTCTCTGCTGCTGCTCCACAGAG 633
Db 624 TGTACCAGCTGTTTCAAGTCTAGCCCTATATCA---TTCTTTGGGATCTGCCATCGAG 680
QY 634 ATATAAAACCAAAATCTTTTGGTTGATCCCAACCCATCAGTGTAAAGTCTGTGATT 693
Db 681 ACATTAACCAACAGAACCTTTGCTGGATCTGTATACAGCTGTATTAAGTCTGCGACT 740
QY 694 TTGGAAGTGCAAAAGTACTGTGGTGAAGGTGAACCAAAACATATATCATATATCTGCTCGGT 753
Db 741 TTGGAAGTGCAAAAGCAGCTGCTGCGAGGAGAGCCCAATGTTTCATATATCTGTTCTCGGT 800
QY 754 ATTACCGAGCTCCAGAACTCATCTTTTGGTGCCACAGAGTATACATCATCATTTGATATAT 813
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QY 814 GGTCTGCTGTTGTTCTGGCAGAGCTACTTCTTGGGAGCGGTTTATTTCCCGGGAGAA 873
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QY 994 GGCATAAGGTTTCCACAGCGGATGCCCTCCGAGGCCATTGACCTTGCATCTCGGCTTC 1053
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Search completed: June 24, 2005, 07:03:27
Job time : 402.52 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 05:27:02 ; Search time 11285.4 Seconds
(without alignments)
6929.914 Million cell updates/sec

Title: X99696
Perfect score: 1614
Sequence: 1 AAGCAAGAGAGAGAAAA.....CCAAAAAAGAGAGAAAAA 1614

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

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2: gb_hcg.*
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12: gb_sy.*
13: gb_un.*
14: gb_vl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1561.4	96.7	1582	8	AY035048
4	1250.2	77.5	1255	8	AY051053
5	972.2	60.2	1636	8	ATASKDZET
6	962	59.6	1591	8	AY094423
7	954.6	59.1	1566	8	AY064020
8	951	58.9	1503	8	AY087542
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15	704	43.6	1738	8	ATASKRNA
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23	594.4	36.8	1581	8	PHPSK4
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ALIGNMENTS

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KEYWORDS	SOURCE	AKS iota gene; shaggy-like kinase iota. Arabidopsis thaliana (thale cress)				
ORGANISM		Arabidopsis thaliana				
REFERENCE	AUTHORS	1 Dornelas,M.C., Schwebel-Dugue,N., Thomas,M., Lechamy,A. and Kreis,M.				
TITLE		Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939 and X99696) (PGR97-008)				
JOURNAL	REFERENCE	Plant Physiol. 113, 306-306 (1997)				
AUTHORS		Dornelas,M.C.				
JOURNAL	TITLE	Direct Submission				
		Submitted (01-AUG-1996) M.C. Dornelas, Universite De Paris-Sud (Parisexil), Institut De Biotechnologie Des Plantes, Lab. Biol. Du Developpement Des Plantes, Batiment 630, F-91405 Orsay Cedex, FRANCE				
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DB	121	CTGCAGCTTCACGACGGCAGCGCTTTGAAACGCCGCTCCTGAATTGGATTTCTGATAAGGAA	180		
QY	181	ATGTCGTGACGTGTTATTGAGGAAATGACGCTGTTACTTGTCATATCATTTCCACTACT	240		
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QY	241	ATAGAGGCAAAAACGGCGAACAAGACGACCAATAGTTACTAGTGTGCTGAGCGGGTTGTT	300		
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QY	601	CAAACTTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGGTTTGGCCACAGAGATGTG	660		
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10198112
2 (bases 1 to 1572)
Piao,H.L., Jang,H.J., Pih,K.T., Lim,J.H., Kang,S.G., Jin,J.B. and
Wang,I.
Direct Submission
Submitted (18-AUG-1997) Plant Molecular Biology and Biotechnology
Research Center, Gyeongsang National University, Chinju 660-701,
Korea

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QY	168	TTCTGATAAGSAAATGTCTG	CAGCTGTTATTGAGGGAAATGACGCTGTTACTGGTTCATAT	227	
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ACCESSION
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VERSION
  AY051053.1 GI:15293238
KEYWORDS
  Arabidopsis thaliana (thale cress)

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ORGANISM

REFERENCE
AUTHORSTITLE
JOURNALREFERENCE
AUTHORSTITLE
JOURNAL

COMMENT

FEATURES
source

gene

CDS

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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1 (bases 1 to 1255)
Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banno, J., Banh, J., Egu, P.,
Lee, J.M., Toriumi, M., Yu, G., Brooks, S., Chao, Q., Chen, H.,
Karlin-Neumann, G., Kim, C., Lam, B., Miranda, M., Nguyen, M.,
Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and
Theologis, A.
Arabidopsis Open Reading Frame (ORF) Clones
Unpublished
2 (bases 1 to 1255)
Yamada, K., Liu, S.X., Pham, P.K., Banno, J., Banno, P., Dale, J.M.,
Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L.,
Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kaniya, A., Karlin-Neumann, G., Kawai, J., Kim, C.,
Koeema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M.,
Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P.,
Southwick, A., Tracy, S.E., Shinozaki, K., Davis, R.W., Ecker, J.R. and
Theologis, A.
Direct Submission
Submitted (02-AUG-2001) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
The RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kaniya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and
sequenced the pUNI (ORF) clones using the RAFL cDNAs: Yamada, K.,
Liu, S.X., Pham, P.K., Banh, J., Banno, P., Dale, J.M., Goldsmith, A.D.,
Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,
Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H.,
Cheuk, R., Jones, P., Karlin-Neumann, G., Kim, C., Koeema, E., Lam, B.,
Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P.,
Southwick, A., Tracy, S.E., Davis, R.W., Ecker, J.R. and Theologis, A.
Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally
to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP
/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis
genome submitted to GenBank.

Location/Qualifiers

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CDS

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polya_site ·
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Qy	271	ACC	ATTAG	TTACAT	GGCTG	GAGGG	TGTTG	CGAC	AGGTT	CANTT	CGG	ATG	TTTTT	TCAG	330									
Db	249	ACC	ATTAG	TTACAT	GGCCG	GAACG	TGTGTT	GGAA	CAGGAT	CA	TT	CGGA	TTG	TAT	CCAG	308								
Qy	331	GGC	AAATG	CTTGG	AAATCTG	GAATCAG	TAGCC	CAATAAAA	AGGCTCT	TG	C	AAAGAT	CGAC	GC	390									
Db	309	GCA	AAATG	CTTGG	AAATCTG	GAATCAG	TAGCC	CAATTA	AGAG	GTGTTG	CG	AGAT	CG	CGCT	368									
Qy	391	TAT	AAAA	ACCGT	GAGTTG	GAACTA	TATG	CGACCA	ATGGAT	CA	CCCA	ATG	TCAT	CT	CTTG	450								
Db	369	TAT	AAAA	ACCG	AGTTG	CAATTA	TATG	CGACTA	TATG	GCACTA	TATG	GCACTA	CCAA	ATG	TGTT	CTTG	428							
Qy	451	AAG	CACTG	TTTCT	CTTCA	ACAG	TATAG	ATGAG	ATGAG	CTCTT	CT	CAAC	CTG	TAT	TGAG	510								
Db	429	AGC	ATTG	TTTCTT	CTTCA	ACAG	CTATAG	ATGAG	ATGAG	CTCTT	CT	CAATCT	CG	TAT	TGAG	488								
Qy	511	TAT	G	TAC	TGAG	CACTTTAT	ACCG	GGTTT	TGAGG	CACTAT	ACT	AGTTCT	TAAT	CAG	AGG	ATG	570							
Db	489	TAT	G	TAC	CAG	AGACAT	TGTAC	CGG	TTT	TGAG	CACTAT	ACT	AGTTCT	TAAT	CAG	AGG	ATG	548						
Qy	571	CCA	ATT	TTCTAT	G	CAAG	CTTTTAC	ATAT	CAAA	ATCTTT	TAG	AGGTTT	GG	CTT	CA	TCAT	630							
Db	549	CCT	AT	CTTAT	G	TG	CAAACTTT	TAC	ATAC	CAAA	ATCTT	CAG	AGCTT	GG	CTT	ATAT	608							
Qy	631	ACT	G	TTCCG	GTGTTG	CCACAG	AGATG	TGA	AAACCA	CAAA	ATCTT	TG	TGTTG	AT	CCCT	TTG	690							
Db	609	ACT	G	TTCT	CGTGT	CTGCC	AGAGATATA	AAACCA	CAAA	ATCTT	TG	TGTTG	AT	CCCT	TTG	668								
Qy	691	ACC	CA	T	CAG	GTTAAG	CTGTG	TCATTT	TGGA	AGTGCA	AAAA	GTAT	TG	TGTT	CGA	AGG	ATG	750						
Db	669	ACC	CA	T	CAG	GTTAAG	CTGTG	TCATTT	TGGA	AGTGCA	AAAA	GTAT	TG	TGTT	CGA	AGG	ATG	728						
Qy	751	AA	CA	TAT	CA	TATAT	CTG	CTCCG	TTAT	TAT	CGT	GCT	CGA	AT	CA	TCAT	CTT	TTG	CGG	CG	CA	810		
Db	729	AA	CA	TAT	CA	TATAT	CTG	CTCCG	TTAT	TAT	CGT	GCT	CGA	AT	CA	TCAT	CTT	TTG	CGG	CG	CA	788		
Qy	811	GAG	TAT	CAG	AGAT	CCAT	AGATAT	TATG	GTCT	GCTG	TGTTG	TGTTG	TGTTG	TGTTG	TGTTG	TGTTG	TGTTG	870						
Db	789	GAG	TAT	CAG	AGAT	CCAT	AGATAT	TATG	GTCT	GCTG	TGTTG	TGTTG	TGTTG	TGTTG	TGTTG	TGTTG	TGTTG	848						
Qy	871	GGC	CA	G	CGCG	CGT	TTATTT	CCAG	GAAAA	ATTCAG	TG	CTCAG	TTG	CTG	GAG	AT	CA	TA	AA	AG	GT	930		
Db	849	GGG	CA	G	CGCG	CGT	TTATTT	CCAG	GAAAA	ATTCAG	TG	CTCAG	TTG	CTG	GAG	AT	CA	TA	AA	AG	GT	908		
Qy	931	CTT	G	TAT	CT	CA	AACT	CTG	TGA	AAATTCG	AT	TG	AT	TG	AA	CCG	AA	CT	CA	CAG	AT	TT	TAG	990
Db	909</																							

Qy	991	TTCCACAAATCAAAGCTCACCCCTTGGCACAGGTTTTTCATAAACCAGATGCTCCACGAA	1050
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Qy	1051	GCAATAGACCTTGCATCTCGGCTCTTTCAATATATCACCAAGTCTACGCTGCACGTGCGCTC	1110
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Qy	1111	GAAGCATGTGCTCATCCGTTTTTCAATGAACCTCGAGAGCCAAACGCCCGCTTTCCAAAT	1170
Db	1089	GAGGCATGTGCGCATCCGTTTTTCAATGAACCTCGTGAGCCAAATGCTCGTCTTCCAAAT	1148
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Qy	1231	CTAATCAACAGGCTTAATACCTTGACGATGTGAGAGCAGCAAAATGAGCAGAGGATACAAAC	1290
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Qy	1291	AGTTAAAAAC-----TGTGCATGCTCTGAAGAGAAAAGAGGAGAAAAG	1331
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Qy	1332	CAGGTTTACTACTTTATTTTATAGTAGTTGACAGGTTTCAACAGTATATTAAACACGACTATT	1391
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Qy	1392	ATCAGCTTCTATACCCCTAGTAAAGTCATATTTCAGCTTTTTTGAAAAATCAGATGCTGATA	1451
Db	1389	AGATGATGTCCTCTCCTTTAGACGTGGCCAAATTCAGCTTTTTTGAGAAATCAGGAGCGCATG	1448
Qy	1452	ATTGCGGTCTATTTTTTTTTTTTATTTCCCTTAGCTGGAGAGTGGAGAGACACTGTTCTCTCG	1511
Db	1449	ATTGTGTCCTCAATATAATCTTTTTTGTTCCTGACTGTGTAGAGAGATCTTTTCTCTCTGTA	1508
Qy	1512	TGTAATTTTTGTATATGTTTTTGTCTGTAAACCAATCTGACAGATACGTAGAGACAAAAG	1571
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Qy	1572	AAAAACGAGGTGATAATTTAAACCAAAAAAANAANAANAANA	1614
Db	1569	AAAAAANAANAANAANAANAANAANAANAANAANAANAANA	1611

9 JUL 1963

AY094423
LOCUS AY094423 1591 bp mRNA linear PLN 05-MAY-2002
DEFINITION Arabidopsis thaliana At3g30980/F7F1.19 mRNA, complete cds.

ACCESSION
AY094423
VERSION
AY094423.1 GT:20453107

VERSION
KEYWORDS
FI054423:1
FI:2043310
FI: CDNA

KEYWORDS
SOURCE
Arabidopsis thaliana (A. thaliana)
FLU CDNA.

SOURCE Arabidopsis thaliana (CHINESE CRESS)
ORGANISM Arabidopsis thaliana

ORGANISM
ARABIDOPSIS THALIANA
Eukaryota: Viridiplantae: Streptocarpales

Eukaryota; Viridiplantae; Streptophyta; Charophyta; Magnoliophyta; Eudicotyledons; Magnoliopsida; Asterales; Gentianaceae; *Streptocarpus*

Spermatophyta; Magnoliophyta; eudicotyledons; rosids; eucomida II; Eucotyledoneae.

rosids; eurosids II; Brassicales;
1 (Lecanodermaceae, 150)

REFERENCE
1 (bases 1 to 1591)

AUTHORS
Shinn, P., Chen, H., Cheuk, R., Kim, C.

Bowser, L., Carninci, P., Chang, E.,

Hayashizaki, Y., Ishida, J., Jones, T.

Kawai, J., Lam, B., Lee, J.M., Lin, J.

Nguyen, M., Onodera, C.S., Palm, C.J.

Satou, M., Seki, M., Southwick, A., T

Yamada, K., Yamamura, Y., Yu, G., Yu,

Theologis, A. and Ecker, J.R.

TITLE Arabidopsis cDNA clones

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1591)

AUTHORS
Shinn, P.; Chen, H.; Cheuk, R.; Kim, C.

Bowser, H., Carninci, P., Chang, E.,

Havashizaki, Y., Ishida, J., Jones, T., Dowse, E., Carmichael, J., Chang, E.,

[illegible]

Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yamamura,Y., Yu,G., Yu,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.

Direct Submission

Submitted (08-APR-2002) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PCEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shinn,P., Chen,H., Cheuk,R., Kim,C.J., Meyers,M.C., Banh,J., Bowser,L., Chang,E., Dale,J.M., Goldsmith,A.D., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yamamura, Y., Yu,G., Yu,S., Davis,R.W., Theologis,A., and Ecker,J.R.

Shinn,P. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk) contributed equally to this work as PIs.

Location/Qualifiers

1. .1591

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/mol_type="mRNA"

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/chromosome="2"

/clone="RAFL05-02-L16 (R21926)"

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80. .1318

/note="putative shaggy-like protein kinase dzeta"

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/protein_id="AA019796.1"

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VTSQRMPLFYVKKLYQIFRGLAYLTHPGVCHRDVKPQNLAVDPLTHOCKLDFG
SAKVLVGEANISYICSBRYRPELIFGATEYTSIDISWAGCVLAEILLQGLPFFGE
NSDVLVEILVLTGPTREERIRCNPNPTDFRFOIKAHPHWFKHRRMPPEAIDLAS
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ORIGIN

Query Match 59.6%; Score 962; DB 8; Length 1591;
Best Local Similarity 78.0%; Pred. No. 3.7e-229;
Matches 1220; Conservative 0; Mismatches 315; Indels 29; Gaps 4

QY 5 AAAGAGAGAGGAAAAATAGACTTTTACTCAATTGTTTCAGTGCTGAGAGAGAAAAGAG-TA 63
DB 14 ATAGAGAGAGAACAAATAGTCTTTACTC---TTTCAGTGAGAGAGAGATTGAGCTG 70

QY 64 AAAAGCAGCATGGCGCTCATTAACCATGGGGCTCAGCCTCATGCTCTTG-----CTCCG 117
DB 71 TAAAGCAGCATGACTTCGATACCATTCAGTGGGGCTCTCTCAGCTCTTAGCTCTCTCAG 130

QY 118 CCGCTGCGAGTTTCAGCAGCGGAGCGCTTTGAAACGCCCGTCTGGAATTGGATTCTGATAG 177
DB 131 CCGCGCGATCTTTCAGCGCGGAGATTCTTTGAAACGTCGTCGCCGATATAGACAAACGACAG 190

QY 178 GAAATGCTCGAGCTGTTATTGAGGGAATGACGCTGTTACTGGTCATATCATTTCCACT 237
DB 191 GAAATGCTGCTGCTGTTATTAGAGGAATGATGCTGTTACGGTCACATATTCTACT 250

QY 238 ACTATAGAGGACAAAACCGCGCAACCAAGCAGACCATTAGTTACATGGCTGAGCGGGTT 297

Db	1331	GAGATGCTTTTCCAGAGCAAAATGCGCCCTTATGGAATGAAGGAGGGAGATTACTTC	1399
Qy	1359	GACAGGTTCAACAGTATATTAACACAGCTATTATTACAGCTTCTATACCGCTAGTAAAGTC	1418
Db	1391	TCTCTGATTAACATAGTATCAGCTTCTGAGAAGAGATGATGTCCTCTTAGACGTGGC	1450
Qy	1419	ATATTACAGCTTTTTCAGAAATCAGATGCTGATTAATTCGCTCTATTTTTTTTATTCCTT	1478
Db	1451	CAATTCAGCTTTTTCAGAAATCAGAGGCGCATGATGTCCTTATTAATATCTTTTGT	1510
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RESULT 7			
LOCUS	AY064020	1566 bp mRNA linear	PLN 18-SEP-2002
DEFINITION	Arabidopsis thaliana putative shaggy protein kinase dzeta (At2g30980) mRNA, complete cds.		
ACCESSION	AY064020.1	GI:17381127	
VERSION	FLI CDNA.		
KEYWORDS	Arabidopsis thaliana		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.		
REFERENCE	1 (bases 1 to 1566)		
AUTHORS	Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.		
TITLE	Arabidopsis Full Length cDNA Clones		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1566)		
AUTHORS	Yamada, K., Banh, J., Banno, F., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-NOV-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA		
COMMENT	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.		
	The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada, K., Banh, J., Banno, F., Chang, E., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H., Cheuk, R., Jones, T., Kamiya, A., Karlin-Neumann, G., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P., Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.		
	Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC) contributed equally to this work as PIs.		

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.			
FEATURES	Location/Qualifiers	source	
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ORIGIN			
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Best Local Similarity	78.1%;	Pred. No. 2.6e-22;	
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Qy	97	CAGCCTCATGC-----TCTTGCTCCGCGCTGCAGCTTCACGACGGGACGCTTTGAAA	150
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Qy	151	CGCGTCTCTGATTTGGATTCTGATAGGAAATGCTCGAGCTTTATTGAGGGAATGAC	210
Db	138	CGTGTCCGATATAGACACGCAAGGAATGTCTGCTGCTTTATAGAGGAATGAT	197
Qy	211	GCTGTTACTGTCATCATTTCCACTACTATAGGAGCAAAAGCGGCAACCAAGCAG	270
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Qy	271	ACCATTAGTTACATGGCTGAGCGGTTGTTGGAACAGGTTTCATTCGGGATTTGTTTCAG	330
Db	258	ACCATTAGTTACATGGCGAAGCTGTTGTTGGAACAGGATCATTCCGAATTTGTTCCAG	317
Qy	331	CGGAATGCTTGGAAACTGGAGATCAGTAGCCATTAAGAGGTCTTGCAGATCGACGC	390
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Qy	391	TATAAAACCGTGAGTTCGAATTAATGCGACCAATGGATCACCCAAATGTCTATCTCTTG	450
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Db	618	ACTGCTCTCTG	TCTGCCACAGAGATGTGAACCAAAATCTCTTGGTTGATCCGCTC	677	
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Qy	811	GAGTATACAG	ATCCATAGATATATGGTCGCTGGTTGTGTACTGTGCAGAGCTTCTTCCT	870	
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Qy	871	GGCGAGCGGT	TTATTTCCAGGAGAAAAATTCAGTTTCATCAGCTCTGTGGAGATCATAAAGGTT	930	
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Qy	931	CTTGGTACTC	CAACTCGTGAAGAAAATTCGATATGTAAGAACCCGAACTATACAGATTTTATAGG	990	
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Qy	1332	CAGGTTTACT	ATTTTATAGTTTGAACAGGTTCAACAGTATATTAAACACGACTATT	1391	
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Qy	1392	ATCAGCTTCT	ATACCCGTAGTAAGTCAATATTGAGCTTTTGGAGAAATCAGATGCTGATA	1451	
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Qy	1452	ATTGCGTCTA	TTTTTTTTTTTTTATTCCTTAGCTCGAGAGTGGAGAGACACTGTTCTCTCG	1511	
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DB 78 CTTACAGCTCCCTCTTTAGCTCTCAGCGCGCGCATCTTTCAGCGCGGAGATTCTTTGAAA 137
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DB 138 CGTGTCCGATATAGACAAACAGCAAGGAATGCTGCTGCTGTTATAGAGGAATGAT 197
QY 211 GCTGTACTGCTCATATCAATTTCCACTACTATAGGAGCAAAACGGCGAAACCAAGCAG 270
DB 198 GCTGTACTGCTCATATCAATTTCTACTCAATTTGAGGCAAAATGCTGAACTTAAACAG 257
QY 271 ACCATTAGTACATGCTGAGCGGTGTTGGAACAGGTTCAATTCGGGATGTTGTTTTCAG 330
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QY 331 GCGAATGCTTGGAACTCGGAATCAGTAGGCATTTAAAGGCTTTGCAAGATCGAGCG 390
DB 318 GCAAAATGCTTGGAACTCGGAATCAGTAGGCATTTAAAGGCTTTGCAAGATCGAGCG 377
QY 391 TATAAAACCGTGAGTTCGAATTAATGCGACCAATGGAATCACCCTCAATGCTATCTCTTG 450
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QY 451 AAGCACTGTTCTTCTCAACAGAGTAGAGCTTCTTCTCAACCTTCTGATGTTATGAGG 510
DB 438 AAGCACTGTTCTTCTCAACAGAGTAGAGCTTCTTCTCAACCTTCTGATGTTATGAGG 497
QY 511 TATGTACCTGAGACTTTATACCGGTTTGGAGCACTATACCTAGTCTTAATCAGAGGATG 570
DB 498 TATGTACCTGAGACTTTATACCGGTTTGGAGCACTATACCTAGTCTTAATCAGAGGATG 557
QY 571 CCAATTTTCTATGCTCAAGCTTTACATATCAATCTTTAGAGGTTTGGCTTACATCCAT 630
DB 558 CCAATTTTCTATGCTCAAGCTTTACATATCAATCTTTAGAGGTTTGGCTTACATCCAT 617
QY 631 ACTGTTCCCGGTGTTGCGACAGAGTAGGAAACCAAAATCTCTTGGTGTGATCCCTTG 690
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QY 691 ACCCATCAGTTAAGCTGTGCTGATTTGGAAGTGCAGAAAGTATTCGTCAAGGTCAGCA 750
DB 678 ACCCATCAGTTAAGCTGTGCTGATTTGGAAGTGCAGAAAGTATTCGTCAAGGTCAGCA 737
QY 751 AACATATCATATATCTGCTCCGCTTATTATCTGCTCCAGAACTCATCTTTGGCGCCACA 810
DB 738 AACATATCATATATCTGCTCCGCTTATTATCTGCTCCAGAACTCATCTTTGGCGCCACA 797
QY 811 GAGTATACAGCATCATAGATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 870
DB 798 GAGTATACAGCATCATAGATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 857
QY 871 GCGCAGCGCTTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGTT 930
DB 858 GCGCAGCGCTTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGTT 917
QY 931 CTTGTGCTCCTCAACTCGTGAAGAAATTCAGTATGTAACCGAACTTACACAGATTTTAGG 990
DB 918 CTTGTGCTCCTCAACTCGTGAAGAAATTCAGTATGTAACCGAACTTACACAGATTTTAGG 977
QY 991 TTCCCAAAATCAAAAGCTCACCTTGGCAAGAGTTTTCATPAAACGAGTCCCTCCAGAA 1050
DB 978 TTCCCAAAATCAAAAGCTCACCTTGGCAAGAGTTTTCATPAAACGAGTCCCTCCAGAA 1037
QY 1051 GCAATAGACTTGCATCTCGGCTTCTCAATATTCAGGATCAGCTAGCTGCACTCGCTC 1110
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QY 1111 GAAGCATGTGCTCATCGCTTTTCAATGAATCCGAGAGCAAAACCGCGTCTTCCAAAT 1170
DB 1098 GAGGCATGTGCGCTCGCTTTTCAATGAATCCGAGAGCAAAACCGCGTCTTCCAAAT 1157

QY 1171 GGTCTCTCATTTACCGCTTGTTCATTTCAAAAGAGTTAGGTGGAGCTTCAATGGAG 1230
DB 1158 GCGCGACCTCTACCGCTTGTTCATTTCAAAAGAGTTAGGTGGAGCTTCAATGGAG 1217
QY 1231 CTAATCAACAGGCTAATACCTGAGCATGTGACGACCAAAATGAGCAGCATTTACAA 1287
DB 1218 CTTATCAACAGGCTAATACCGCTTGTTCATTTCAAAAGAGTTAGGTGGAGCTTCA 1274

RESULT 9
AY096698 1270 bp mRNA linear PLN 18-SEP-2002
LOCUS Arabidopsis thaliana putative shaggy protein kinase dzeta
DEFINITION (A2930980) mRNA, complete cds.
ACCESSION AY096698
VERSION AY096698.1 GI:20465726
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (chale cress)
ORGNISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 1270)
AUTHORS Yanada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
Tang, C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,
Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
Arabidopsis Open Reading Frame (ORF) Clones
Unpublished
TITLE 2 (bases 1 to 1270)
JOURNAL Yanada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M.,
REFERENCE Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L.,
AUTHORS Tang, C.C., Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L.,
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,
Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J.,
Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A.,
Shinozaki, K., Davis, R.W., Ecker, J.R. and Theologis, A.
Direct Submission
TITLE Submitted (16-APR-2002) Plant Gene Expression Center, 800 Buchanan
JOURNAL Street, Albany, CA 94710, USA
COMMENT The RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.
The Salk, Stanford, PGE (SSP) Consortium members constructed and
sequenced the PUNI (ORF) clones using the RAFL cDNAs: Yanada, K.,
Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M.,
Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C.,
Toriumi, M., Wu, H.C., Yamamura, Y., Yu, G., Bowser, L., Chen, H.,
Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Lam, B.,
Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P.,
Southwick, A., Davis, R.W., Ecker, J.R. and Theologis, A.
Yanada, K. (SSP/PGE) and Seki, M. (RIKEN GSC) contributed equally
to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP
/PGE) contributed equally to this work as PI8.

Annotation is based on the January 2002 version of the Arabidopsis
genome submitted to GenBank.
FEATURES
Location/Qualifiers
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/clone="U11538"

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Qy	404	AGTTGCAACTAATCGGACCAATGGATCAACCAATGTCTCTCTTGAAGCACTGTTTCT	463
Db	242	AACTTCAGTTGATGCGGTGTGATGGATCATCCGAATGTGGTTGTTTGAAGCATTGCTTCT	301
Qy	464	TCTCTACAAACGAGTAGAGATCAGCTCTTCCTCAACCTTGTATATGGAGTAGTGTACTCTGAGA	523
Db	302	TTTCGACTACAGTAAAGACGAGCTTTTCTGAACTTGTTATGGAGTAGTGTCCCTGAGA	361
Qy	524	CTTTATACCGGGTTTTGAGGCACTATACTAGTTCTTAATCAAGAGTAGCCAAATTTTCTATG	583
Db	362	GCTGTATCGAGTTCTGAAACATTTATAGTAGTGCAAACCAAGAAATGCTCTGTGCTATG	422
Qy	584	TCAAGCTTTTACACATATCAAACTTTTAGAGGTTTTGGCTTACATCCATACTGTTCCCGGTG	643
Db	422	TTAAACTTTTACATGTATCAGATCTTCGGGGAGCTTGTCTTACATTCACAAGTTGTCTGGAG	481
Qy	644	TTTGCCACAGAGATGTGAACCCACAAATCTCTTGTTGTATGCTTGACCCCATCAGGTTA	703
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Qy	704	AGCTGTGTGATTTTTGGAAGTSCAAAAAGTATTGGTCAAAAGGTGAACCAACAATATCATATA	763
Db	542	AAATCTGTGACTTTGGCAGTSCGAAACAGCTCGTTAAAGGTGAAGCCAAATTTCTTACA	601
Qy	764	TCTGCTCCCGTTATTATCGTGCTCCAGAACTCATCTTTTGGCGGCCACAGAGTAGTACAGAT	823
Db	602	TCTGCTCACGATCTACCGTGCACCCGAGCTCATATTTGGTGGCCACTGAGTACACAAT	661
Qy	824	CCATAGATATATGCTGTGCTGGTTGTGTACGCGAGAGCTTCTTCTTGGCCAGCGTTAT	883
Db	662	CTATTGATATCTGCTGTGCTGGTTGTGTCTTGTCTGAGCTTCTTCTTGGTCAAGCANTAT	721
Qy	884	TTCCAGGAGAAAAATTGACTGTGATCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCAA	943
Db	722	TTCCGGAGAAAAATGCTGTGGATCAGCTCGTTGAAATTTATAAAAGTTCTTGGTACACAA	781
Qy	944	CTCGTGAAGAAATTCGATGTATGAACCGGACTACACAGATTTTAGGTTCCCACAATCA	1003
Db	782	CTCAGAGAAATCCGTTGTATGAATCCACATTAACAGATTTTCAAGGTTTCCACAGATAA	841
Qy	1004	AAGCTCACCCCTTGGCACAAGGTTTTTATATAACCGGATGCCCTCCAGAAAGCAATAGACCTG	1063
Db	842	AGGCACATCCCTGGCACAAGATCTTCCAAAAAGGATGCCCCCAAGAGCGATGATTTTG	901
Qy	1064	CATCTCGGCTTCTTCAATATTTCAACAGATCTACGCTGACGTGCGCTCGAAGCATGTGCTC	1123
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Qy	1124	ATCCGTTTTTCAATGAACCTCGAGAGCCAAACGCCGCTCTTCCAAATGGTGTGCTCCATTAC	1183
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Qy	1184	CGCCATTGTTCAATTTTCAACAAGAGTTTAGTGGAGCTTCAATGGAGCTTAATCAACAGGC	1243
Db	1022	CGCTCTCTTCACTTCAACAAGAGTAGTGTGATCATCACCTGAATGGTCAACAGT	1081
Qy	1244	TAATACCTGAGCATGTGAGACGACAAATATGACACAGGATT	1283
Db	1082	TGATTTCAAGACCATATCAAGAGACAAATGGGTCTTAAGCTT	1121

RESULT 11	
AX506180	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	

AX506180	1143 bp	DNA	linear	PAT 27-SEP-2002
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AX506180
1143 bp
Sequence 875 from Patent WO0216655.

Sequence 875 FROM Patient
AX506180

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QY 944 CTCGTGAAGAAATTCATGTATGAACCCGAACTACACAGATTTAGTTTCCACAAATCA 1003
Db 782 CTCGAGAGAAATCCGTTGTATGAATCCACATTTACACAGATTTTCAGGTTTCCACAGATA 841
QY 1004 AAGCTCACCTTGGCAAGAGTTTTCATAAAGCGATGCTCCAGAAAGCAATAGACCTTG 1063
Db 842 AGGCAATCCCTGGCAAGATCTCCAAAGAGATGCCCCAGAAAGCATGATTTG 901
QY 1064 CATCTCGGCTTCTTCAATATTCACCAAGTCTAGCTGCTGCTCGAGCATGTGCTC 1123
Db 902 CATCAAGGCTGCTTCAATACTCTCAAGTCTAAGATGCACAGGCTCGAAGCTTTGTCAC 961
QY 1124 ATCCGTTTTCATGAACCTCGAGAGCCAAACGCCGCTCTTCAATGTGCTGCATTAAC 1183
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QY 1184 CGCATTGTTCAATTTCAACAGAGTTAGTGGAGCTTCAATGGAGCTTAATCAACAGGC 1243
Db 1022 CGCCTCTCTTCAACTTCAACAGAGATGAGTGGATCATCAGCTGAAGTGGTCAACAGT 1081
QY 1244 TAATACCTGAGCATGTGAGACGACCAATGAGCACAGGATT 1283
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RESULT 12

AY086529
LOCUS AY086529
DEFINITION Arabidopsis thaliana clone 256076 mRNA, linear PLN 14-APR-2003
ACCESSION AY086529
VERSION AY086529.1 GI:21405239
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 1636)
Haas,B.J., Volkovskiy,N., Town,C.D., Troukhan,M., Alexandrov,N.,
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
Genome Biol. 3 (6), RESEARCH0029 (2002)
22088475
PUBMED 12093376
REFERENCE 2 (bases 1 to 1636)
Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Full-length cDNA from Arabidopsis thaliana
Unpublished
3 (bases 1 to 1636)
Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Direct Submission
Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
Malibu, CA 90265, USA
This clone sequence is one of 5,000 Ceres full-length cDNAs made
available to TIGR and Genbank. The following quality assessment of
this set was done by comparison with known proteins; two percent of
the clones are estimated to be 5'-truncated; less than one percent
are 3'-truncated; approximately two percent represent alternative
splice variants, including unspliced introns and spliced exons; one
percent may contain premature stop codons; five percent may have
frame shifts in a coding region. A sequence is considered to be
5'-truncated if it lacks the translation initiation start (ATG). A
sequence is considered to be 3'-truncated if it lacks the
C-terminal end of the encoded protein. Please note that these cDNA
sequences are derived from the Ws or Laer ecotypes and therefore
may contain polymorphisms when compared to sequences from Col-0.
Genset carried out the library production and sequencing of the

full-length clones. Ceres, Inc. carried out the clustering of the
5' sequences, selection of clones, and sequence assembly.

FEATURES

source location/Qualifiers

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VCHRDLPQNLLVDPLTHQVKICDFGSARQLVKGBANISYICSRFYRACMLFPGATEY

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FPQIKAHPWKIFHKRMPPEDAFASRLIQVSPSLRCTALEACAHFPFDELREPNAFL

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ORIGIN

Query Match 44.0%; Score 710.4; DB 8; Length 1636;

Best Local Similarity 77.1%; Pred. No. 2.5e-166;

Matches 864; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 164 TCGATTCTGATAAGAAATGCTGCAGCTGTTATTGAGGGAATGACGCTGTACTGTC 223

Db 174 TGGCTGATGAAGAGATGCTGCTGCTGTAGTTGATGGACATGATCAAGTCACCTGGTC 233

QY 224 ATATCATTTCCACTACTATAGGAGGCAAAACGGGCAACCAAGAGCAGACCATTAGTTACA 283

Db 234 ATATTATTTCCACCAACATCGTGGCAAAATGTTGAAACCAACAGACATTAGTTACA 293

QY 284 TGGCTGAGCGGTTGTTGGAACAGGTTTATTTCGGGATGTTTTCAGGCGAAATGCTTGG 343

Db 294 TGGCGAGCGGTTGTTGGTACAGGCTCTTCGGGATCGTTTTTCCAAAGCAAAATGTTGG 353

QY 344 AACTGGGAATCAGTAGCCATTAAAGAGTCTTCAAGATCGAGCTATAAAACCGTG 403

Db 354 AGACTGGGAACACCGTGGCGGATAAAGAGTTTTCAGATAGAGATCAAGAACCGAG 413

QY 404 AGTTGCAACTAATGGCAACCAATGGATCACCCAAATGTCATCTCTTGAAGCACTGTTCT 463

Db 414 AACTTCAGTTGATCGGTGATGGATCATCCGATGTTGTTTGAAGCATGCTTCT 473

QY 464 TCTCTAACAGAGTAGAGATGAGCTTCTCTCAACCTTGTATGGAGTAGTACCTGAGA 523

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Db 654 TTTGTACACAGAGATCTAAAGCGCTCAAAATCTTCTGTTGATCTCTTACTCATCAAGTCA 713

QY 704 AGCTGTGTATTTTGAAGTGCAGAAAGTATTGGTCAAGGTGAACCAACATATCATATA 763

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Db 774 TCTGCTCAGATTCATCCGTGACCCGAGCTCATATTGTTGGTCCACTGAGTACACAACTT 833

QY 824 CCATGATATATGCTGCTGTTGTGTATCTGGCAGAGCTTCTTCTTGGCCAGCGGTTAT 883

Db 834 CTATTGATATCTGGTCTGCTGTTGTGTTCTTCTTGGAGCTTCTTCTTGGTTCAGCCATTAT 893

Qy	884	TTCCAGGAGAAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCAA	943
Db	894	TTCCCGGAGAAAATTCGCTGTGATCAGCTCGTTGAAATTTATAAAAGTTCTTGGTACACCAA	953
Qy	944	CTCGTGAAGAAAATTCGATGTATGAACCGGACTACACAGATTTTAGTTGCCCAAAATCA	1003
Db	954	CTCAGGAAGAAAATTCGGTTGTATGAATCCATTAACACAGATTTTCAGGTTTCCACAGATAA	1013
Qy	1004	AAGCTCACCCCTTGGCACAAGAGTCTTTTTCATAAACGGATCGCTCCAGAAAGCAATAGACCTTG	1063
Db	1014	AGGCACATCCCTGGCACAAGATCTTCACAAAAGGATGCCCCAGAGAGCGATTGATTG	1073
Qy	1064	CATCTCGGCTTCTTCAATATATTCACAAAGTCTACGCTGCACATGCGCTCGAAGCATGTGCTC	1123
Db	1074	CATCAAGGCTGCTTCAATATCTCTCAAGTCTTAAGATGCACAGCGCTCGAAGCTTGTGCGAC	1133
Qy	1124	ATCCGTTTTTCAATGAAGTCCGAGAGCCAAAGCGCGCTCTTCCAAAATGGTGTGCTCATATC	1183
Db	1134	ATCCGTTCTTTGATGAATCTCAGAGAACCAAAAGCTCGCTTTACCAAAATGGAGCGGCTTTCC	1193
Qy	1184	CGCCATTGTTTCAATTTCAAAACAGAGTTAGTGTGAGCTTCAATGGAGCTTAATCAACAGGC	1243
Db	1194	CGCTCTCTTCACTTCAACACAGAGTAGCTGATCATCACTGAACTGGTCAACAGT	1253
Qy	1244	TAATACCTGAGCATGTGAGACGCAAAATGAGCACAGGATT	1283
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RESULT	13
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LOCUS	Arabidopsis thaliana AT4g18710/P28A21_120 mRNA linear PLN 18-FEB-2002
DEFINITION	Arabidopsis thaliana AT4g18710/P28A21_120 mRNA, complete cds.
ACCESSION	AY075699
VERSION	AY075699.1 GI:18700187
KEYWORDS	FLI CDNA.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS	Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
TITLE	Arabidopsis cDNA clones
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1670)
AUTHORS	Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
TITLE	Direct Submission
JOURNAL	Submitted (25-JAN-2002) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
COMMENT	RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, P0EC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shinn,P., Chen,H., Cheuk,R., Kim,C.J., Meyers,M.C., Banh,J., Bowser,L., Chang,E., Dale,J.M., Goldsmith,A.D., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yamamura, Y., Yu.G., Yu.S., Davis,R.W., Theologis,A., and Ecker,J.R.

Shinn,P. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk) contributed equally to this work as PIs.

Location/Qualifiers
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 VCHRDUKPNQLLDPLTHQVKICDFGSARQLVKGEANISYICSRPFRAPRELIFGATEY
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misc_difference 1150
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ORIGIN

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 AKI02147
 ACCESSION
 VERSION AKI02147.1 GI:32987356
 KEYWORDS FLI_CDNA; CAP trapper.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1
 AUTHORS The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Iizuka,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuka,K., Shishiki,T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Ohtsuka,K., Tada,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Kuroaki,T., Kodama,T., Masuda,H., Kobayashi,M., Xie,Q., Lu,M., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Miura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., RIKEN, Kawai,J., Carninci,P., Adachi,J., Aizawa,K., Arakawa,T., Fukuda,S.,

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

Hara,A., Hashidume,W., Hayatsu,N., Imotani,K., Arakawa,T., Carninci,P., Doi,K., Kagawa,I., Kondo,S., Konno,H., Miyazaki,A., Osato,N., Ota,Y., Saito,R., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Yoshino,M. and Hayashizaki,Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
 Science 301 (5631), 376-379 (2003)
 22752273
 12869764
 2 (bases 1 to 1863)
 Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Doi,K., Fujimura,T., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashizaki,Y., Hayatsu,N., Hiramoto,K., Iizuka,M., Hori,F., Hotta,I., Iida,Y., Ikeda,R., Imamura,K., Imotani,K., Ishibiki,J., Ishii,Y., Iehikawa,M., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawagashira,N., Kawai,J., Kawamata,M., Kikuchi,S., Kishikawa-Hirozane,T., Kishimoto,N., Kobayashi,M., Kodama,T., Kojima,K., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Kurosaki,T., Kusumegi,T., Li,C., Lu,M., Masuda,H., Matsubara,K., Matsuyama,T., Miura,J., Miyazaki,A., Mizuno,K., Murakami,K., Murata,M., Nagata,T., Nakamura,M., Namiki,T., Narikawa,R., Niikura,J., Nishi,K., Nomura,K., Numasaki,R., Ohneda,E., Ohno,M., Ohtsuki,K., Oka,M., Ooka,H., Osato,N., Ota,Y., Ohtsuka,K., Ohta,H., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Satoh,K., Shibata,K., Shinagawa,A., Shiraki,T., Shishiki,T., Sogabe,Y., Sugano,S., Sugiyama,A., Suzuki,K., Suzuki,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toyota,T., Tsunoda,Y., Ueda,M., Waki,K., Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J., Yokomizo,S. and Yoshimura,A.
 Direct Submission
 Submitted (27-AUG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

TITLE
 JOURNAL

This clone is one of the 28K full-length cDNA clones from japonica rice.
 URL : http://cdna01.dna.affrc.go.jp/cDNA/NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuka,K., Shishiki,T. and Yamamoto,M.
 PALS Genome Sequencing & Analysis Group: Ohtsuka,Y., Iida,Y., Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M., Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J., Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagami-Takeda,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toyota,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.

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FEATURES
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ORIGIN

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DEFINITION			
ACCESSION	X94939		
VERSION	X94939.1	GI:1161511	
KEYWORDS	ASK etha gene; shaggy-like kinase etha.		
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi			
REFERENCE	1 Dornelas,M.C., Schwebel-Dugue,N., Thomas,M., Lecharny,A. and Kreis,M.		
AUTHORS	Three New cDNAs Related to SGG/GSK-3 (SHAGGY/Glycogen Synthase Kinase-3) from Arabidopsis thaliana (Accession No. X94938, X94939 and X99696) (PGR97-008)		
TITLE	Plant Physiol. 113, 306-306 (1997)		
JOURNAL	2 (bases 1 to 1738)		
REFERENCE	Dornelas,M.C.		
AUTHORS	Direct Submission		
TITLE	Submitted (10-JAN-1996) M.C. Dornelas, UNIVERSITE de Paris-Sud,		
JOURNAL	Institut de Biotechnologie des Plantes, Centre de Recherches sur les Plantes, URA 1128, Biol.du Devel.des Plantes, Bat.630, F-91405 ORSAY Cedex, FRANCE		
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Query Match			
Best Local Similarity			
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Qy      1124 ATCCGTTTTCATAGAACTCCGAGAGCCAAACGCCGCTCTTCCAAATGGTTCGTCATTAC 1183
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 03:29:55 ; Search time 1265.83 Seconds
(without alignments)
7547.973 Million cell updates/sec

Title: X99696

Perfect score: 1614

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870657 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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5: Geneseqn2001bs.*

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10: Geneseqn2003cs.*

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12: Geneseqn2004as.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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14	678.8	42.1	1621	8 AAC57970	Aac57970 Canola pr
15	672.8	41.7	1653	3 AAC48014	Aac48014 Zea mays
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ALIGNMENTS

RESULT 1

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XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 34186.

KW Hybridisation assay; genetic mapping; gene expression control;

KW protein identification; signal transduction pathway; metabolic pathway;

KW promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-00301439.

PR 25-FEB-1999; 99US-0121825P.

PR 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

PR 16-APR-1999; 99US-0129845P.

PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

PR 23-APR-1999; 99US-0130510P.

PR 28-APR-1999; 99US-0131449P.

PR 30-APR-1999; 99US-0132048P.

PR 30-APR-1999; 99US-0132407P.

PR 04-MAY-1999; 99US-0132484P.

PR 05-MAY-1999; 99US-0132485P.

PR 06-MAY-1999; 99US-0132486P.

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35	523.4	32.4	1429	5 AAH47003	Aah47003 Soy bean
36	523.4	32.4	1429	6 ABQ82533	Abq82533 Soybean g
37	516.8	32.0	1757	8 ACC57969	Acc57969 Canola pr
38	503	31.2	1654	8 ACC57971	Acc57971 Canola pr
39	496.8	30.8	1296	6 ABZ12869	Abz12869 Arabidops
40	496.8	30.8	1296	6 ADG87959	Adg87959 A. thalia
41	496.8	30.8	1296	12 ADN73136	Adn73136 Thale cre
42	400	24.8	1100	8 ACC57961	Acc57961 Protein k
43	397.4	24.6	608	13 ACN53505	Acn53505 Cotton an
44	385.2	23.9	1230	10 ADK66952	Adk66952 Gene #42
45	385.2	23.9	1389	4 AAD11491	Aad11491 Human gly

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FT	WO2003040171-A2.	/product= "GmpK-3"	
XX	15-MAY-2003.		
XX	12-NOV-2002; 2002WO-US036374.		
XX	09-NOV-2001; 2001US-0346096P.		
PR	(BADI) BASF PLANT SCI GMBH.		
XX	Van Thielens N, Da Costa E SilvaO, Chen R;		
XX	WPI: 2003-441522/41.		
DR	P-PSDB; ABR42368.		
XX	New protein kinase stress-related polypeptide coding nucleic acid, useful		
PT	for producing transgenic plants with an increased tolerance to an		
PT	environmental stress, e.g. high salinity, as compared to a wild type		
PT	variety of the plant.		
XX	Claim 1; Page 96-97; 111pp; English.		
XX	The present sequence is a full-length cDNA encoding GmpK-3, a novel		
CC	soybean protein kinase stress-related polypeptide (PKSRP). The cDNA was		
CC	identified on the basis of homology to Physcomitrella patens PK-3 (see		
CC	ACC57962) and PK-10 (see ACC57966) sequence. GmpK-3 is an example of		
CC	PKSRPs of the invention that are important for modulating a plant's		
CC	response to environmental stress. Over-expression of PKSRP coding nucleic		
CC	acids in a plant results in the plant's increased tolerance to		
CC	environmental stress. Transgenic monocot and dicot plants are provided		
CC	that show increased tolerance to high salinity, drought and low		
CC	temperature		
XX	Sequence 1744 BP; 502 A; 379 C; 380 G; 483 T; 0 U; 0 Other;		
SQ	Query Match 47.3%; Score 763.2; DB 8; Length 1744;		
	Best Local Similarity 78.6%; Pred. No. 1.3e-195;		
	Matches 912; Conservative 0; Mismatches 248; Indels 0; Gaps 0;		
QY	115 CCGCCGCTGCAGTTCACGACGCGAGCTTTGAAACGCGCTCCTGAATGGATTCGTAT 174		
DB	112 CCGCCGCTGCAGTTCACGACGCGAACCGAAGTTCTCTCGCGGAGCTCCGATGTGGAGACCGAT 171		
QY	175 AAGGAATGCTCAGCTGTATTGAGGGAATGACGCTGTACTGGTCATATCATTTCC 234		
DB	172 AAGGATATGTCAGCTACTGTCAATTGAGGGAATGATGCTGTCACTGGCCACATAATCTCC 231		
QY	235 ACTACTATAGGAGGCAAAACCGCGAACCAAGACAGACCATTAATGATTACATGGCTGAGCGG 294		
DB	232 ACCACAATTTGGAGGCAAAATGGGAACCTTAAGAGACCATCACTGATTACATGGCAGAACGT 291		
QY	295 GTTGTGGAAACAGGTCATTCGGGATGTTTTTTTCAGCGGAAATGCTTTGGAAATCGGAGAA 354		
DB	292 GTTGTGGCACTGGATCATTTGGAGTTGTTTTTCAGSCAAAGTGTCTGGAGACTGGAGAA 351		
QY	355 TCAGTAGCCATTAAGAGTCTTTCAGAGATCGAGCTATTAAGACCGTGGATTGCAACTA 414		
DB	352 GCAGTGGCTATTAAAGAGTCTTTCAGAGACAGCGGTTACAAATAATCGTAATTCGAGTTA 411		
QY	415 ATCGGACCAATGGATCACCATAATGTCATCTCTTGAAGCAGCTGTTCTCTCTACAACG 474		
DB	412 ATCGGCTTAATGGATCACCATAATGTAATTTCTCTGAGCAGCTGTTCTCTCCACACA 471		
QY	475 AGTAGAGATGAGCTCTTCTCTCAACCTTTGATAGGATGATGATCCTGAGACTTTATACCGG 534		
DB	472 AGCAGAGATGAATCTTTTCTAAACTTGGTAATGGAATATGTTCCCGAATCAATGATACCGA 531		
QY	535 GTTTTGGAGCACTATAGTCTTATATCAGAGATGCCAATTTCTATGTCAGACTTTAC 594		
DB	532 GTTATAAGCACTACACTACTATGTAACCAAGAGAATGCCCTCTCATCTATGTGAACACTGTAT 591		
QY	595 ACATATCAAAATCTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGGTGTTTCCACACAGA 654		
DB	592 ACATATCAAAATCTTTAGGGGATTAGCATATATCCATACCGCACTGGAGTTTGGCCATAGG 651		
QY	655 GATGTAAACCAACAAAATCTCTTGGTTGATCCCTTGACCCCATCAGGTTAAGCTGTGTGAT 714		
DB	652 GATGTAAAGCCTCAAAAATCTTTTGGTTTCATCTCTTACTCACCAGATTAAAGCTATGTGAT 711		
QY	715 TTTTGAAGTGCAGAAAGTATTGGTCAAGGTAACCAACATATCATATATCTGCTCCCGT 774		
DB	712 TTTGGAGTGCAGAAAGTCTTGGTCAAGGTAATCAACATTTTCAATATATGTTTCAAGT 771		
QY	775 TATTATCGTGTCTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGCATCCATAGATATA 834		
DB	772 TACTATCGGGCTCCAGAACTAATAATTGGTGCAACAGAAATACACAGCTCTCTATTGATATC 831		
QY	835 TGGTCTGCTGGTTGTGTTACTGGCAGAGCTTCTTCTTGGCCAGCGGTTATTTCCAGAGAA 894		
DB	832 TGGTCAGCTGGTTGTGTTCTTCTGTAACCTTCTTAGGACAGCCATTAATTTCTCGAGAA 891		
QY	895 AATTCAAGTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCCAACTCGTGAAGAA 954		
DB	892 AACCAAGTGGACCAACTTGTGGAATTTCAAGGTTCTTGGTACTCCAACTCGGAGGAA 951		
QY	955 ATTGATGTATGAACCCGAACTACACAGATTTTAGGTTCCCAAAATCAAAAGCTCACCCCT 1014		
DB	952 ATCCGTTGTATGAACCCAAATTTATACAGAGTTTATAGATTCCTCAGATTAAAGCTCATCT 1011		
QY	1015 TGGCAAGAGTTTTCATTAAGCGATGCTCCAGAAAGCAATAGACCTTGCATCTCGGCTT 1074		
DB	1012 TGGCAAGAGTTTTCACCAAGCGAATGCTCTGGAAGCAATTTGACCTTGCATCAAGGCTT 1071		
QY	1075 CTTCAATATTCACCAAGTCTACGCTGCACTGGCTCGAAGCATGTGCTCATCGTTTTC 1134		
DB	1072 CTCGAATATTCACCTAGTCTCCGCTGCACTGGCTGGAAGCATGTGCACTCTTCTTCTT 1131		
QY	1135 AATGAATCTCGAGAGCCAAACGCCGCTCTTCCAAATGGTCCCATTAACGCCATTTGTTTC 1194		
DB	1132 GATGAGCTTCGCGAACCAATGCCCGGTACCTAATGGCGCTCCACTGCCCCACCTTTTC 1191		
QY	1195 AATTTCAAAACAGAGTTAGTGGAGTTCAATGGAGCTTAATCAACAGGCTAATACCTGAG 1254		
DB	1192 AACTTTCAACAGAGTTAGTGGAGCATCACCTGAACTGATCAATAGGCTCATCCAGAG 1251		
QY	1255 CATGTGAGACGACAAATGAG 1274		
DB	1252 CATATTAGCGCGAGATGGG 1271		
RESULT 5			
AAC47997			
ID	AAC47997 standard; DNA; 1657 BP.		
XX	AAC47997;		
AC	18-OCT-2000 (first entry)		
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 55886.		
DE	Arabidopsis thaliana.		
XX	EP1033405-A2.		
PN	06-SEP-2000.		
XX	25-FEB-2000; 2000EP-00301439.		
PF	25-FEB-1999; 99US-0121825P.		
XX	05-MAR-1999; 99US-0123180P.		
PR	Hybridisation assay; genetic mapping; gene expression control;		
KW	protein identification; signal transduction pathway; metabolic pathway;		
KW	promoter; termination sequence; ss.		
XX	Arabidopsis thaliana.		

PR 09-MAR-1999;	99US-0123548P.	PR 15-JUL-1999;	99US-0144005P.
PR 23-MAR-1999;	99US-0125788P.	PR 16-JUL-1999;	99US-0144085P.
PR 25-MAR-1999;	99US-0126264P.	PR 16-JUL-1999;	99US-0144086P.
PR 29-MAR-1999;	99US-0126785P.	PR 19-JUL-1999;	99US-0144325P.
PR 01-APR-1999;	99US-0127462P.	PR 19-JUL-1999;	99US-0144331P.
PR 06-APR-1999;	99US-0128234P.	PR 19-JUL-1999;	99US-0144332P.
PR 08-APR-1999;	99US-0128714P.	PR 19-JUL-1999;	99US-0144333P.
PR 16-APR-1999;	99US-0129845P.	PR 19-JUL-1999;	99US-0144334P.
PR 19-APR-1999;	99US-0130077P.	PR 19-JUL-1999;	99US-0144335P.
PR 21-APR-1999;	99US-0130449P.	PR 20-JUL-1999;	99US-0144352P.
PR 23-APR-1999;	99US-0130510P.	PR 20-JUL-1999;	99US-0144352P.
PR 23-APR-1999;	99US-0130891P.	PR 20-JUL-1999;	99US-0144884P.
PR 28-APR-1999;	99US-0131449P.	PR 21-JUL-1999;	99US-0144814P.
PR 30-APR-1999;	99US-0132048P.	PR 21-JUL-1999;	99US-0145086P.
PR 30-APR-1999;	99US-0132407P.	PR 21-JUL-1999;	99US-0145088P.
PR 04-MAY-1999;	99US-0132484P.	PR 22-JUL-1999;	99US-0145085P.
PR 05-MAY-1999;	99US-0132485P.	PR 22-JUL-1999;	99US-0145087P.
PR 06-MAY-1999;	99US-0132486P.	PR 22-JUL-1999;	99US-0145089P.
PR 06-MAY-1999;	99US-0132487P.	PR 22-JUL-1999;	99US-0145192P.
PR 07-MAY-1999;	99US-0132863P.	PR 23-JUL-1999;	99US-0145145P.
PR 11-MAY-1999;	99US-0134256P.	PR 23-JUL-1999;	99US-0145218P.
PR 14-MAY-1999;	99US-0134218P.	PR 23-JUL-1999;	99US-0145224P.
PR 14-MAY-1999;	99US-0134219P.	PR 26-JUL-1999;	99US-0145276P.
PR 14-MAY-1999;	99US-0134221P.	PR 27-JUL-1999;	99US-0145913P.
PR 14-MAY-1999;	99US-0134370P.	PR 27-JUL-1999;	99US-0145918P.
PR 18-MAY-1999;	99US-0134768P.	PR 27-JUL-1999;	99US-0145919P.
PR 19-MAY-1999;	99US-0134941P.	PR 28-JUL-1999;	99US-0145951P.
PR 20-MAY-1999;	99US-0135124P.	PR 02-AUG-1999;	99US-0146386P.
PR 21-MAY-1999;	99US-0135353P.	PR 02-AUG-1999;	99US-0146388P.
PR 24-MAY-1999;	99US-0135629P.	PR 02-AUG-1999;	99US-0146389P.
PR 25-MAY-1999;	99US-0136021P.	PR 03-AUG-1999;	99US-0147038P.
PR 27-MAY-1999;	99US-0136392P.	PR 04-AUG-1999;	99US-0147204P.
PR 28-MAY-1999;	99US-0136782P.	PR 04-AUG-1999;	99US-0147302P.
PR 01-JUN-1999;	99US-0137222P.	PR 05-AUG-1999;	99US-0147192P.
PR 03-JUN-1999;	99US-0137528P.	PR 05-AUG-1999;	99US-0147260P.
PR 04-JUN-1999;	99US-0137502P.	PR 06-AUG-1999;	99US-0147303P.
PR 07-JUN-1999;	99US-0137724P.	PR 06-AUG-1999;	99US-0147416P.
PR 08-JUN-1999;	99US-0138094P.	PR 09-AUG-1999;	99US-0147493P.
PR 10-JUN-1999;	99US-0138540P.	PR 09-AUG-1999;	99US-0147935P.
PR 10-JUN-1999;	99US-0138847P.	PR 10-AUG-1999;	99US-0148171P.
PR 14-JUN-1999;	99US-0139119P.	PR 11-AUG-1999;	99US-0148319P.
PR 16-JUN-1999;	99US-0139452P.	PR 12-AUG-1999;	99US-0148341P.
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PR 17-JUN-1999;	99US-0139492P.	PR 13-AUG-1999;	99US-0148684P.
PR 18-JUN-1999;	99US-0139454P.	PR 16-AUG-1999;	99US-0149368P.
PR 18-JUN-1999;	99US-0139455P.	PR 17-AUG-1999;	99US-0149175P.
PR 18-JUN-1999;	99US-0139456P.	PR 18-AUG-1999;	99US-0149426P.
PR 18-JUN-1999;	99US-0139457P.	PR 20-AUG-1999;	99US-0149722P.
PR 18-JUN-1999;	99US-0139458P.	PR 20-AUG-1999;	99US-0149723P.
PR 18-JUN-1999;	99US-0139459P.	PR 20-AUG-1999;	99US-0149929P.
PR 18-JUN-1999;	99US-0139460P.	PR 23-AUG-1999;	99US-0149902P.
PR 18-JUN-1999;	99US-0139461P.	PR 23-AUG-1999;	99US-0149930P.
PR 18-JUN-1999;	99US-0139462P.	PR 25-AUG-1999;	99US-0150566P.
PR 18-JUN-1999;	99US-0139463P.	PR 26-AUG-1999;	99US-0150884P.
PR 18-JUN-1999;	99US-0139750P.	PR 27-AUG-1999;	99US-0151065P.
PR 18-JUN-1999;	99US-0139763P.	PR 27-AUG-1999;	99US-0151066P.
PR 21-JUN-1999;	99US-0139817P.	PR 30-AUG-1999;	99US-0151080P.
PR 22-JUN-1999;	99US-0139899P.	PR 30-AUG-1999;	99US-0151303P.
PR 23-JUN-1999;	99US-0140353P.	PR 31-AUG-1999;	99US-0151438P.
PR 23-JUN-1999;	99US-0140354P.	PR 01-SEP-1999;	99US-0151930P.
PR 24-JUN-1999;	99US-0140695P.	PR 07-SEP-1999;	99US-0152363P.
PR 28-JUN-1999;	99US-0140823P.	PR 10-SEP-1999;	99US-0153070P.
PR 29-JUN-1999;	99US-0140991P.	PR 13-SEP-1999;	99US-0153758P.
PR 30-JUN-1999;	99US-0141287P.	PR 15-SEP-1999;	99US-0154018P.
PR 01-JUL-1999;	99US-0141842P.	PR 16-SEP-1999;	99US-0154039P.
PR 01-JUL-1999;	99US-0142154P.	PR 20-SEP-1999;	99US-0154779P.
PR 02-JUL-1999;	99US-0142055P.	PR 22-SEP-1999;	99US-0155139P.
PR 06-JUL-1999;	99US-0142390P.	PR 23-SEP-1999;	99US-0155486P.
PR 08-JUL-1999;	99US-0142803P.	PR 24-SEP-1999;	99US-0155659P.
PR 09-JUL-1999;	99US-0142920P.	PR 28-SEP-1999;	99US-0156458P.
PR 12-JUL-1999;	99US-0142977P.	PR 29-SEP-1999;	99US-0156596P.
PR 13-JUL-1999;	99US-0143542P.	PR 04-OCT-1999;	99US-0157117P.
PR 14-JUL-1999;	99US-0143624P.	PR 05-OCT-1999;	99US-0157533P.

PT producing plants with increased tolerance to these abiotic stresses.
 PS Claim 144; SEQ ID NO 875; 577bp + Sequence Listing; English.
 CC The invention relates to identifying a stress condition to which a plant
 CC cell has been exposed, comprising: (a) contacting nucleic acid
 CC representative of expressed polynucleotides in the plant cell with an
 CC array or probes representative of the plant cell genome; and (b)
 CC detecting a profile of expressed polynucleotides in the plant cell
 CC characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 CC with increased tolerance to abiotic stress. The present sequence is that
 CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
 CC in methods of the invention. Note: The sequence data for this patent is
 CC not represented in the printed specification but is based on sequence
 CC information supplied to Derwent by the European Patent Office
 XX
 XX Sequence 1143 BP; 323 A; 245 C; 247 G; 328 T; 0 U; 0 Other;
 Query Match 44.0%; Score 710.4; DB 6; Length 1143;
 Best Local Similarity 77.1%; Pred. No. 2.1e-181;
 Matches 864; Conservative 0; Mismatches 256; Indels 0; Gaps 0;
 QY 164 TCGATTCTGATAAGAAATGCTGCGAGCTGTTATTGAGGGAATGACGCTGTACTGGTC 223
 DB 2 TGGCTGATGAAGAGATGCTGCTGCTGTAGTGTGATGACATCAAGTCACTGGTC 61
 QY 224 ATATCATTTCCACTACTATAGGAGGCAAAACCGGCAACCAAGCAGACCATTAGTTACA 283
 DB 62 ATATTATTCCACCACATCGTGGCAAAATGTTGACCAACCAAGCAGACCATTAGTTACA 121
 QY 284 TGGCTGAGCGGTTGTTGGAACAGGTTCAATCGGATGTTTTTTCAGGCGAAATGCTGG 343
 DB 122 TGGCGAGCGAGTGTGTTGTAAGGCTGTTCCGGATCGTTTTTCCAAAGCAAAATGTTGG 181
 QY 344 AAACCTGGAGAACTAGTACGATTAAGAGTCTTCAAGATCGAGCTATTAAGACCGTG 403
 DB 182 AGACTGGAGAAACCGTGGGATGAAGAGGTTTGAAGATGAAGATGAAGAACCGAG 241
 QY 404 AGTTGCAACTTAATGCGAACCAATGGAATCAACCAATGTCATCTCTTGAAGCACTGTTCT 463
 DB 242 AACTTCAGTTGATGCTGTGATGATCCGAAATGCTGTTGTTGAAGCATGCTTCT 301
 QY 464 TCTTACACAGATGAGATGAGCTTCTTCCCAACCTGTTATGAGATGATGACCTGAGA 523
 DB 302 TTTCGACTACAGTAAAGACGAGCTTTCTTGAACCTTGGTTATGAGTATGCTCCCTGAGA 361
 QY 524 CTTTATACCGGTTTGGAGCACTATAGTCTTAATCAGAGGATGCCAATTTCTATG 583
 DB 362 GCTTGTATCGAGTTCTGAACCAATTATAGTAGTGAACCAAGAAATGCTCTTGTCTATG 421
 QY 584 TCAAGCTTTACATATCAAACTTTTAGAGGTTTGGCTTACATCCTATCTGTTCCGGTG 643
 DB 422 TTAACCTTTACATGATGATCTTCCGGGACTGCTTACATTCACATGTTGCTGGAG 481
 QY 644 TTTGCCACAGAGATGTAACCAACCAAAATCTCTTGGTTGATCCCTTGACCCCATCAGGTTA 703
 DB 482 TTTGTCACAGAGATCTAAGACCTCAAAAATCTTCTGTTGATCCTCTTACTCATCAAGTCA 541
 QY 704 AGCTGTGATTTTGGAGTGAAGTGAAGTATGTTGTCAGAGTGAACCAACATATCATATA 763
 DB 542 AAATCTGTGACTTTGGCAGTGGCAACAGCTCGTTAAAGGTTGAAGCCCAATTTCTTACA 601
 QY 764 TCTGCTCCCGTTATTATGCTGCTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGAT 823
 DB 602 TCTGCTCAGACTTACCGTGCACCGAGCTCATATTTGGTGCCACTGAGTACACAACTT 661
 QY 824 CCATGATATATGCTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 883
 DB 662 CTAATTGATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 721
 QY 884 TTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGTCTTGTGTTACTCCAA 943

DB 722 TTCCTGGAGAAATCTGCTGGATCAGCTGTTGAAATATATAAAGTTCTTGTGTACACCAA 781
 QY 944 CTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTTAGTTTCCCAAAATCA 1003
 DB 782 CTCGAGAAAGAAATCCGTTGTATGAATCCACATTCACAGATTTTCAAGTTTCCACAGATA 841
 QY 1004 AGCTCACCTTGGCACAAGGTTTTTTCATAACGATGCTCCAGAGCAATAGACCTTG 1063
 DB 842 AGGCACATCTCCCTGGCACAAGATCTTCCAAAGAGTCCCTCCAGAGCGATTTGATTTG 901
 QY 1064 CATCTCGGCTTCTCAATATTCCCAAGTCTACGCTGCACTCGCTCGAAGCATGTGCTC 1123
 DB 902 CATCAAGGCTGCTTCATATCTCCAGTCTTAAGATGACAGCGTTCGAGGTTGTGCAC 961
 QY 1124 ATCCGTTTTTCAATGAATCCGAGAGCCAAACCGCTGTTTCCAAATGCTGCTCATATAC 1183
 DB 962 ATCCGTTCTTGTGATGAATCAGAGAAACCAACGCTGTTTACCAATGAGCGCTTTCC 1021
 QY 1244 TAATACCTGAGCATGTGAGAGCAAAATGAGCAGCAGGATT 1283
 DB 1082 TGATTCAGACATATCAAGAGCAATTTGGTCTAAGCTT 1121
 RESULT 7
 ADN73384
 ID ADN73384 standard; cDNA; 1143 BP.
 XX
 AC ADN73384;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Thale cress cDNA upregulated in E2Fa/Dpa expressing plants SeqID 1279.
 XX
 KW gene; ss; plant; transgenic; E2Fa/Dpa transcription factor;
 KW growth regulator; animal feed product; thale cress;
 KW cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO2004035798-A2.
 XX
 PD 29-APR-2004.
 XX
 PF 20-OCT-2003; 2003WO-EP011658.
 XX
 PR 18-OCT-2002; 2002EP-00079408.
 XX
 PA (CROP-) CROPDISEGN NV.
 XX
 PI Inze D, De Veylder L, Vlieghe K;
 XX
 DR WPI; 2004-348466/32.
 DR P-PSDB; ADN73385.
 XX
 PT Altering plant characteristics, useful for producing plants for enzyme or
 PT pharmaceutical production comprises modifying in a plant, expression of
 PT one or more nucleic acids and/or modifying level or activity of one or
 PT more proteins.
 XX
 PS Claim 1; SEQ ID NO 1279; 134pp; English.
 XX
 CC This invention relates to a novel method for altering one or more plant
 CC characteristics. Specifically, it refers to identifying genes that are up
 CC - or down-regulated in transgenic plants overexpressing the heterodimeric
 CC E2Fa/Dpa transcription factor of Arabidopsis and using these sequences to
 CC alter plant characteristics accordingly. The present invention describes
 CC generating transgenic plants for the production of growth regulators,
 CC enzymes, therapeutics, pharmaceuticals and animal feed products, where
 CC the altered plant characteristics are selected from increased yield or

CC	biomass, enhanced survival capacity, stress tolerance, plant architecture
CC	or physiology, altered endoreduplication, biochemistry, signal
CC	transduction, storage lipid mobilisation and/or altered photosynthesis,
CC	each relative to the corresponding wild type plants. Accordingly, these
CC	sequences can also be useful as positive or negative selectable markers
CC	during transformation of cells or tissues. The identified genes play a
CC	role in a variety of biological processes such as DNA replication, cell
CC	wall biosynthesis, nitrogen and/ or carbon metabolism or they function as
CC	transcription factors. This polynucleotide sequence is the cress cDNA
CC	upregulated 1.3 fold or more in plants overexpressing the E2Fa/Dpa
CC	transcription factor, given in an exemplification of the invention.
XX	
SQ	Sequence 1143 BP; 323 A; 245 C; 247 G; 328 T; 0 U; 0 Other;
Query Match 44.0%; Score 710.4; DB 12; Length 1143;	
Best Local Similarity 77.1%; Pred. No. 2.1e-181;	
Matches 864; Conservative 0; Mismatches 256; Indels 0; Gaps 0;	
QY	164 TGGATTCTGATAGGAAATGCTGCGAGCTGTTATTGAGGGAATGACGCTGTACTGGTC 223
DB	
QY	2 TGGCTGATGATAGGAGATGCCCTGCTGCTGTAGTTCATGACATGATCAAGTCACCTGGTC 61
DB	
QY	224 ATATCAATTTCCACTACTATAGGAGGCAAAACGGCGAACCAAGCAGACATTAAGTTACA 283
DB	
QY	62 ATATTATTTCCACCACCAATCGGTGGCAAAATGCTGAACCAAAACAGACAATTAGTTACA 121
DB	
QY	284 TGGCTGAGCGGGTGTGGACAGGTTCAATTCGGGATGTTTTCAGGCGAATGCTTGG 343
DB	
QY	122 TGGCGGAGCGAGTGTGTGGTACAGGCTGCTGCTGCGGATCGTTTCCAGCAAAATGTTGG 181
DB	
QY	344 AAACCTGGAGAAATCAGTAGCCATTAATAAGGCTCTTCAAGATCGACGCTATATAAAACCGTG 403
DB	
QY	182 AGACTGGAGAAACCGTGGCGATAAGAGGTTTTCAGATAGAAATACNAGAACCGAG 241
DB	
QY	404 AGTTGCAACTAATGCGACCAATGGATCACCCAAATGTCACTCTTCTTGAAGCACTGTTTCT 463
DB	
QY	242 AACTTCAGTTGATGCGTGTGATGGATCATCCGAATGTGGTTGTTTGAAGCACTGCTTCT 301
DB	
QY	464 TCTCTACACGAGTAGAGTAGCTCTTCTCAACCTGTTGATGGAGTAGTACCTGAGA 523
DB	
QY	302 TTTGGAAGTACAAGTAAGACGAGCTTTTCTTGAACCTTGGTTATGGAGTAGTCCCTGAGA 361
DB	
QY	524 CTTTATACCGGGTTTGGAGCACTATAGTTCTAATCAGAGATGCCAAATTTTCTATG 583
DB	
QY	362 GCTTGTATCGAGTTCTGAAACATATATAGTAGTCAAAACCAAGATGCTCTTGTCTATG 421
DB	
QY	584 TCAAGCTTTACATATCAAACTTTAGAGGTTTGGCTTACATCCATATGTTCCCGGTG 643
DB	
QY	422 TTAACCTTTTACATGATATCAGATCTCCGGGGAAGTCTTCAATTCACAATGTTGCTGGAG 481
DB	
QY	644 TTTGCCACAGAGATGTGAAACCAACCAAAATCTCTTGGTGTGATCCCTTGACCCATCAGTTA 703
DB	
QY	482 TTTGTACAGAGATCTAAGAGCCCTCAAAATCTCTGTTGATCTCTTACTCATCAAGTCA 541
DB	
QY	704 AGCTGTGTGATTTTGGAAAGTGCAAAATGTTTGTGTAAGGTGAACCAACATATCATATA 763
DB	
QY	542 AAATCTGTGACTTTGGCAGTGCAGAACACAGCTCGTTAAAGGTGAAGCCACATTTCTTACA 601
DB	
QY	764 TCTGCTCCCGTTATATATGCGTCCAGAACTCAATCTTTTGGCGCAACAGAGTATACAGCAT 823
DB	
QY	602 TCTGCTCACGATTTCTACCGGTGCAACCGAGCTCATATTTGGTGGCACTGAGTACACAACCT 661
DB	
QY	824 CCATAGATATATGCTGCTGGTGTGTGATCTGTCAGAGGCTTCTTCTTGGCGAGCGCTTAT 883
DB	
QY	662 CTATGATATATCTGGTCTGGTGTGTGTTCTTCTGCTGAGCTTCTTCTTGGTCAGCCATTAT 721
DB	
QY	884 TTTCCAGAGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCCAA 943
DB	
QY	722 TTCCCGGAGAAATGCTGTGATCAGCTCGTTGAAATATATAAGTTCTTGGTACACCAA 781
DB	
QY	944 CTGCTGAAGAAATTCGATGATGAACCCGAACTACACAGATTTAGTTTCCCAACAATCA 1003
DB	
QY	782 CTCGAGAAGAAATCCGTTGTATGAATCCATTTACACAGATTTTCAGGTTTCCACAGATTA 841
DB	

QY	1004 AAGCTCACCTTGGCACAGAGGTTTTTTTATAACCGATGCTCCAGAGCAATAGACCTTG 1063
DB	
QY	842 AGGCACATCCCTGGGCACAGATCTTCCACAAAGAGATGCCCCAGAGCGATGATTTTG 901
DB	
QY	1064 CATCTCGGCTTCTTCAATATTCCCAAGTCTACGCTGCACTCGCTCGAAGCATGTGCTC 1123
DB	
QY	902 CATCAAGGCTGCTTCAATACTCTCCAAAGTCTAAGATGCACAGCGCTCGAAGCTTGTGCAC 961
DB	
QY	1124 ATCCGTTTTTCAATGAACCTCCAGAGCCAAACCGCGTCTTCCAAATGCTGCTCCATTAC 1183
DB	
QY	962 ATCCGTTCTTTGATGAACCTCAGAGAACCAACCGCTCGTTTACCAATGACGCGCTTTC 1021
DB	
QY	1184 CCCCATTTGTTCAATTTCAACCAAGAGTGTAGGTGGAGCTTCAATGGAGCTTAATCAACAGGC 1243
DB	
QY	1022 CCGCTCTCTTCACTTCAACCAAGAGTGTAGTGTGATCATCACTGATGCTGATGCTGATCAAGT 1081
DB	
QY	1244 TAATACCTGAGCATGTGAGACGACCAAAATGAGCACAGGATT 1283
DB	
QY	1082 TGATTCAGACCATATCAAGAGACAAATTTGGTCTAAGCTT 1121
DB	
RESULT 8	
AAL54221	
ID	AAL54221 standard; cDNA; 1490 BP.
XX	
AC	AAL54221;
XX	
DT	27-MAR-2003 (first entry)
XX	
DE	cDNA of wild-type DWf12 protein.
XX	
KW	DWf12; DWf12; transgenic plant; plant breeding; industrial application;
KW	agricultural production; gene; ss.
XX	
OS	Unidentified.
XX	
EH	Location/Qualifiers
CDS	200..1312
FT	/tag= a
FT	/product= "Protein of wild-type DW12 locus"
XX	
PN	WO200292777-A2.
XX	
PD	21-NOV-2002.
XX	
PF	15-MAY-2002; 2002WO-US015563.
XX	
PR	16-MAY-2001; 2001US-0291342P.
XX	
PA	(ARIZ-) ARIZONA BOARD OF REGENTS.
XX	
PI	Choe S, Feldmann K, Tax F;
XX	
DR	WPI; 2003-129285/12.
DR	P-PSDB; AAO26726, AAO26727.
XX	
PT	New isolated DWf12 mutant polypeptide for producing transgenic plants
PT	displaying altered biochemistry, structure or morphology which are useful
PT	in plant breeding, in agricultural production or industrial applications.
XX	
PS	Example 2; Fig 2; 62pp; English.
XX	
CC	The invention relates to an isolated DWf12 (DWf12) mutant polypeptide.
CC	The mutant polypeptide comprises at least 70 % sequence identity to the
CC	amino acid sequence of the DWf12 polypeptide given in the specification
CC	at positions 38-326 or 1-380, and having a mutation of at least one non-
CC	conservative substitution, addition or deletion of an amino acid in a
CC	region of the polypeptide corresponding to a region given in the
CC	specification. The mutant DWf12 polypeptide is useful in producing
CC	transgenic plants that display at least one altered DWf12 phenotype, such
CC	as altered biochemistry, structure or morphology. The transgenic plant
CC	can be used in plant breeding or directly in agricultural production or

PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139453P.
PR 18-JUN-1999; 99US-0139452P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
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PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 21-JUN-1999; 99US-0139899P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140895P.
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PR 28-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142230P.
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PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
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PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
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PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 04-AUG-1999; 99US-0147038P.
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PR 06-AUG-1999; 99US-0147303P.
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PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
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PR 16-AUG-1999; 99US-0149368P.
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PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
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PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 06-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
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PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
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PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match		44.0%;	Score 710.4;	DB 3;	Length 1745;
Best Local Similarity		77.1%;	Pred. No. 2.5e-181;	Indels 0;	Gaps 0;
Matches 864;		Conservative	0;	Mismatches 256;	
QY	164	TGATTTCTGATAGGAAATGTCTGACGCTGTTATTGAGGGAATACGCGTGTACTGGTC	223		
DB	174	TGCTGATGATAGGAGATGCTGCTGCTGTGTAGTTGATGGACATGATCAAGTCACTGGTC	233		
QY	224	ATATCATTTTCCACTACTATAGAGGCAAAACGGGCAACAAAGCAGACCATTAAGTTACA	283		
DB	234	ATATTATTTCACCAACATCGGTGGGCAAAATGTTGAAACCAACAGCAATTAAGTTACA	293		
QY	284	TGGCTGACGGGCTTCTGGAACAGGTTCAATTCGGGATGTTTTCAGGCGAATGCTTGG	343		
DB	294	TGGCGAGCGAGTTGTGGTACAGGCTGTTCCGGGATCGTTTTCCAGCAAAATGTTGG	353		
QY	344	AAACTGGAGAAATCAGTAGCCATTAATAAGGCTCTGCAAGATCGAGCTATAAAACCGTG	403		
DB	354	AGACTGGAGAAACCTGGGATAGAGAGTTTTCGAGATAGAGATACAGAACCGAG	413		
QY	404	AGTTGCAACTAATGCAACCAATGGATGATCCCAAAATGTCTCTCTGAGCACTGTTCT	463		
DB	414	AACTTCAGTTGATGCTGTGATGGATCATCCGAATGTGGTTGTTGAAGCAATGCTTCT	473		
QY	464	TCTCTACACGAGTAGAGATGAGCTTCTCCTCAACCTTGTATGAGATGTACCTGAGA	523		
DB	474	TTTCGACTACAAAGTAAAGACGAGCTTTTCTTGAACCTTGTGTTATGAGATGTCCCTGAGA	533		
QY	524	CTTTATACCGGTTTGGGCACTACTACTAGTCTTAATCAGAGGATGCCAATTTTCTATG	583		
DB	534	GCTTGTATCGAGTTCTGAAACATTAATAGTAGTGCACCAAGAAATGCTCTTGTCTATG	593		
QY	584	TCAGCTTTTACACATATCAAAATCTTTAGAGGTTTGGCTTTACATCCATCTGTTCCCGGTG	643		
DB	594	TTAAACTTTTACATGATCAGATCTTCCGGGACTTGTCTTACATTCACAAATGTTCTGGAG	653		
QY	644	TTTGCCACAGAGATGTAACACCAAAATCTCTTGGTGTATGATCCCTTGACCCATCAGTTA	703		
DB	654	TTTGTACAGAGATCTAAAGCCCTCAAAATCTTCTGGTTGATCCTCTTACTCATCAAGTCA	713		
QY	704	AGCTGTGTGATTTTGGAGTGAAGATATTCGTCAAGGTGAACCAACATATCATATA	763		
DB	714	AAATCTGTGACTTTGGGAGTGGCAACAGCTCGTTAAAGGTGAGCCAACTTTCTTACA	773		
QY	764	TCTGCTCCGTTTATATCGTGTCCAGAACTCATCTTTGGGCCACAGAGTATACAGAT	823		
DB	774	TCTGCTCAGGATTTACCGTGCACCGAGCTCATATTTGGTGCCTACTGAGTACACAAT	833		
QY	824	CAATAGATATATGCTGCTGCTGTGTGTACTGGCAGAGCTTCTTCTGGCCAGCCGTTAT	883		
DB	834	CTATTGATATCTGGTCTGCTGTGTGTGTCTTCTGCTGAGCTTCTTCTGTCAGCCATTAT	893		
QY	884	TTCCAGGAGAAATTCAGTTGATCAGCTGTGAGATCATAAAGTCTTGTGACTCCAA	943		
DB	894	TTCCCGGAGAAATCTGTGGATCAGCTGTGTGAAATATATAAAGTCTTGTGACACCA	953		
QY	944	CTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTTGGTTTCCACAAATCA	1003		
DB	954	CTCGAGAGAAATCCGTTGTATGAATCCACATTAACACAGATTTTCCAGATATA	1013		
QY	1004	AAGCTCACCTTGGCAGCAAGGTTTTTTCATAACGATGCTCCAGAGCAATAGACCTTG	1063		
DB	1014	AGGCACATCCCTGGCAGCAAGATCTTCCCAAAAGGATGCCCCCAGAGCGATTGATTG	1073		
QY	1064	CATCTCGGCTTCTCAATATTCACCAAGTCTAGCTGCACTGCGCTCGAAGCATGTGCTC	1123		
DB	1074	CATCAAGGCTGCTTCAATACTCTCAAGTCTAAGATGCACAGCGCTCGAAGCTTGTGAC	1133		
QY	1124	ATCCGTTTTTCAATGAACCTCCGAGCCCAACCGCCGCTTCTCAATAGTGTGCTCCATTAC	1183		
DB	1134	ATCCGTTTTTCAATGAACCTCCGAGCAACCAACGCTGTTTACCAATAGGACCGCTTCC	1193		
QY	1184	CGCCATTGTTCAATTTTCAACAAAGATTTAGTGGAGCTTCAATGAGGCTTAATCAACAGGC	1243		
DB	1194	CGCTCTCTTCACTTCACTTCAACAAAGATTTAGTGGATCATCTACCTGATCTGCTCAACAGT	1253		
QY	1244	TAATACCTGAGCATGTGAGACGCAAAATGAGCAGCAGGATTT	1283		
DB	1254	TGATTTCCAGACATATCAAGAGACAATTTGGTCTAAGCTT	1293		
RESULT 10					
AAH47004					
ID	AAH47004	standard;	cDNA;	1673 BP.	
XX	AAH47004;				
AC	AAH47004;				
XX	29-OCT-2001	(first entry)			
DE	Wheat glycogen synthase kinase-3 cDNA.				
KW	Protein kinase; calcium-dependent phosphorylase kinase; CDPK; GSK-3;				
OS	Triticum aestivum.				
FT	Key	Location/Qualifiers			
FT	CDS	44..1252			
FT	/tag=	a			
FT	/product=	"wheat GSK-3"			
XX	US262345-B1.				
XX	17-JUL-2001.				
XX	02-JUL-1999;	99US-00347801.			
XX	10-JUL-1998;	98US-0092438P.			
XX	(DUPO) DU PONT DE NEMOURS & CO E I.				
XX	Allen SM, Lee J;				
XX	WPI; 2001-440863/47.				
XX	P-PSDB; AAB85589.				
XX	New isolated polynucleotide encoding polypeptide having glycogen synthase kinase activity or its complement, useful for producing transgenic plants with altered levels of glycogen synthase kinase.				
XX	Claim 3; Col 45-48;	42pp; English.			
XX	The invention relates to protein kinases, especially calcium-dependent phosphorylase kinase (CDPK) and glycogen synthase kinase-3 (GSK-3). The polypeptides having GSK activity can be expressed by standard recombinant methodology. The polynucleotides encoding the polypeptides are useful for isolating cDNAs and genes encoding homologous proteins from the same or other plant species, for immunological screening of cDNA expression libraries, and for creating transgenic plants in which the glycogen synthase kinase polypeptides are present at higher or lower levels than normal or in cell types or developmental stages in which they are normally found. The polynucleotides are also useful as probes for genetically and physically mapping the genes that they are part of, and as markers for traits linked to those genes. The polypeptides are useful for altering the level of expression of GSK-3 in a transformed host cell.				
XX	The present sequence represents a wheat GSK-3 cDNA				
SQ	Sequence 1673 BP;	419 A;	421 C;	408 G;	424 T; 0 U; 1 Other;
Query Match	43.5%;	Score 701.6;	DB 5;	Length 1673;	
Best Local Similarity	74.7%;	Pred. No. 5.9e-179;			
Matches 881;	Conservative	0;	Mismatches 299;	Indels 0;	Gaps 0;
QY	98	AGCTCATGCTTCTGCTCGCGCTGACGCTTCAAGCGGCGACGCTTTGAACCCGTC	157		
DB	48	AGCATCCGCGCGCGCGCGCGATGCTGCTGACGAGCGCCGCCACCCGAGTCG	107		

Qy	158	CTGAATTTGGAAATCTGATATAAGAAATGCTCGAGCTGTATTGAGGGGAAATGACGCTGTTTA	217
Db	108	CCTCGGAGAAAGACACAGATGGCGAGCGCGTATGCGGAGGGGAAACGACGCCATGA	167
Qy	218	CTGGTCATATCATTTTCCACTACTATAGGAGGCAAAACCGGAACCAAAACGACGACCAATTA	277
Db	168	CCGGTCATCATCTCTCACCAACATCGCGGCAAGAAACGGCGAGCCCAAGCAGACGATTA	227
Qy	278	GTTCATATGGCTGAGCGGGTTGTGGAAACAGTTTCATTCGGGATGTGTTTTTCAGCGCAAAAT	337
Db	228	GCTACATGGCGGAGCGGTTGTGGGCACTGGTTCGTTTGGCATCGTCTTTCAGGCTAAAT	287
Qy	338	GCTTTGAAACTGGAGAAATCAGTAGCCCAATATAAAAGAGTCTTTCGAAGATCGAGCTATAAAA	397
Db	288	GCCTGGAAACCGGGGAGATGTTGGGCATTAAGAAGGTACTCTGCAGGACAGACGGTCAAGA	347
Qy	398	ACCGTAGTTGCCACTAATCGGACCAATGGATCACCCAAATGTCATCTCTCTTGAAGCACT	457
Db	348	ACCGTAGCTGCGAGCTTATGGTTTCGAATGATCCATTCAAATGTTGTTCTCCCTCAAGCACT	407
Qy	458	GTTTCTTCTCTCAACGAGTAGAGATGAGCTCTTCTCAACCTTTGTTATGGAGTATGTAC	517
Db	408	GCITCTTCTCAACCAAGTAGAGATGAGCTGTTCTCTGAACTTGTCTATGAGTATGTCC	467
Qy	518	CTGAGACTTTATACCGGGTTTGGGCACTATATCTAGTTCTTAATCAGAGATGCCAAATTT	577
Db	468	CGGAGACGCTATACCGCGTGCTTAAGCACTACAGTAATGCGCAACACGAGGATGCGCGTTA	527
Qy	578	TCTATGTCAAGCTTTACACATATCAAAATCTTTAGAGGTTTGGCTTACATCCATACTCTTC	637
Db	528	TCTATGTCAAGCTTTATGTAICAGCTTTTATAGGGGCTAGCTTATGTTTCATATCTGTC	587
Qy	638	CCGGTGTTTGCCACAGAGATGTGAACCAACAAATCTCTTGGTTGATCCCTTGACCCATC	697
Db	588	CAGGAGTTTGCCACAGGGATGTGAACCAACAAATGTTTGTGTTGATCTCTTAACCCATC	647
Qy	698	AGTTTAAGCTGTGTGATTTTGGAAAGTCCAAAAGTATTGGTCAAAAGGTGAACCAACATAT	757
Db	648	AAGTCAAGACTCTGTGACTTTTGGAAAGTCCAAAAGTCTCTGTAACCTGGTGAACCCCAACATAG	707
Qy	758	CATATATCTGCTCCGTTATTATCGTCTCCAGAACTCATCTTTGGCGGCCACAGAGATATA	817
Db	708	CATACATATGCTCTCGCTACTATCGTCTCTCTGAGCTCATATTTTGGTGAACATGAATATA	767
Qy	818	CAGCATCCATAGATATATGTTCTGCTGGTTGTGTACTGGCAGAGCTTCTTCTTGGCCAGC	877
Db	768	CAACTTCAATAGACATATGTTTCAGCTGGATGTGTTCTTTGCAGAGCTACTTCTTTGGTCAGC	827
Qy	878	CGTTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGTTCCTTGTA	937
Db	828	CTCTGTTTCCAGGAGAGACTCGCGTTGATCAGCTAGTGGAGATTTATCAAGGTTCTTCTGTA	887
Qy	938	CTCCAACTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTTATAGGTTCCCAAC	997
Db	888	CTCCAAACCGGTGAGAAATTCGGTGCATGAACCCCAACTATACCGAGTTCAGGTTTCTCTC	947
Qy	998	AAATCAAAGCTCACCTCTGGCACAAAGTTTTTTCATAAACCGATGCCTCCGAAAGCAATAG	1057
Db	948	AGATTAAGGCTCATCTCTTGGCACAAAGATTTTCCAAAGAGAAATGCCCGCTGAAGCTATAG	1007
Qy	1058	ACCTTGCATCTCGGCTTCTTCAATATTTTCCACCAAGTCTACGCTGCACTGCGCTCGAAGCAT	1117
Db	1008	ATCTTGGCTCCCGCTTCTCCAGTATTTTCCACCAATCTACGTTGCACTGCTCTTGTATGCAT	1067
Qy	1118	GTGCTCATCCGTTTTTCAAATGAACTCCGAGAGCCAAACGCCGCTCTTCCAAATGGTGCCTC	1177
Db	1068	GTGCACATTCCTTCTTGTAGAGCTAGTGAGCCGAATGACAGCTTGCCGAATGCCGCC	1127
Qy	1178	CATTACCGCCCATGTTCAATTTCAAAACAAGAGTTAGTGGAGCTTCAATGGAGCTAATCA	1237
Db	1128	CATTCCCTCTCTGTTCATCTTCAAACTGAACCTAGGGAACGCCCTCTCCAGAGCTATCA	1187

Qy	1238	ACAGGCTAATACCTGAGCATGTGAGACGACAAATGAGCAC	1277
Db	1188	ACAGGCTTGTTCGGAAACATGTCGACGGCAGAAATGGCCC	1227

RESULT 11
ABQ82534

ID ABO82534 standard: CDNA: 1673 BP.

AC ABQ82534;

DT 19-DEC-2002 (first entry)

DE wheat glycogen synthase kinase encoding cDNA SEQ ID NO:15.

KW Glycogen synthase kinase; kinase; enzyme; plant; immunological screening;

KW plant breeding; gene; ss.

OS *Triticum aestivum*.

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	CDS	44.	.1252

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FT  /*tag= a
    /tag= a
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FT yy /product= "glycogen synthase kinase

PN US2002120949-A1.
yy

PD 29-AUG-2002.
yy

14-MAY-2001; 2001US-00854/31.
PF
yy

PR 10-JUL-1998; 98US-0092438F.
 PR 02-JUN-1999; 98US-00347801

PK 02-000-1555;
XX 5505-0034/801.

PA (ALLEN) ALLEN S M.
XXXX
FI
ATTN SM;

DR WP1; Z00Z=131384/13.
DR P-PSDB: ABP53636.

XX XX
 1950-1951

PT polypeptides, for altering level of expression of kinase polypeptides in plants.

XX
CS 113, Page 22-22, 11/27/2011

dependent phosphorylase kinase polypeptide comprising a sequence of 101, 623, 157 or 111 (see ABP5329 to ABP5362) amino acids, and a glycogen synthase kinase polypeptide comprising all or a portion of a sequence of 410, 105, 399 or 402 (see ABP5363 to ABP5366) amino acids. (I) is useful for immunological screening of cDNA expression libraries, and for preparing antibodies against the polypeptides, where the antibodies would be useful for detecting (I) *in situ* or *in vitro*, in cell extracts. Nucleic acids (II) encoding (I) can be used to isolate cDNAs and genes

CC encoding homologous proteins from the same or other plant species. (II)
CC can also be used for creating transgenic plants in which (II) is present
CC at higher or lower levels than normal or in cell types or in
CC developmental stages in which they are not normally found. (II) are
CC useful as probes or primers. The polynucleotides may be used as probes
CC for genetically and physically mapping the genes that they are a part of
CC and used as markers for traits linked to those genes. The information can
CC be used in plant breeding in order to develop lines with desired
CC phenotypes. The present sequence encodes a glycogen synthase kinase from
CC the present invention
xx

20
sequence 10/3 BF; 413 H; 421 C; 400 G; 424 I; 0 0; 1 0000

Query Match 43.5%; Score 701.6; DB 6; Length 1673;

Best Local Similarity 74.7%; Pred. No. 5.9e-179;

Matches 881; Conservative 0; Mismatches 299; Indels 0; Gaps 0;

QY 98 AGCTCATGCTCTTCTCGCGCGCTGACGCTTACGAGCGGACGCTTTTGAACGCCGTC 157
DB 48 AGCATCCGCGCGCGCGCGCGCGATGCTCTCGAGGAGCGCCCCCACCAGTCG 107
QY 158 CTGAATTCGATCTCTGATAGGAAATGTCTGACGCTGTTATTGAGGGAATAGACGCTGTTA 217
DB 108 CTTGCGAGAGAGCAGCAGGATGCGAGGCGCGTATGCGGAGGGAACGAGCCCATGA 167
QY 218 CTGGTCATATCTTCCACTACTATAGGAGGCAAAACGGCGAACAAGAGCAGCATTATTA 277
DB 168 CCGGTTCATATCTTCCACCATCTCGCGCGCAAGACGGCGAGCCCAAGCAGACGATTA 227
QY 278 GTTACATGCTGAGCGGTTGTTGAACAGGTTTCAATTCGGGATCTCTTTTTCAGGCGAAT 337
DB 228 GCTACATGGCGAGCGCTTGTGGGCACTGGTTCGTTTGGCATCTCTTTTTCAGGCTAAT 287
QY 338 GCTTGAACCTGGGAATCAGTAGCATTAAAGGCTTTCGAAGATCCAGCTATAAAA 397
DB 288 GCCTGGNAACCGGGAGATGTTGGGCAATTAGAAGGTACTGCAGGACAGCGGTACAGA 347
QY 398 ACCGTGAGTTGCACTAATGCGACCAATGGATACCCAAATGTCTATCTCTTGAAGCACT 457
DB 348 ACCGTGAGTGCAGCTTATGCTTCGATGATCCATTCCAAATGTTGCTCTCCCTCAAGCACT 407
QY 458 GTTCTCTCTACACGAGTAGAGATGAGCTCTTCTCAACCTTGTATGAGTATGTAC 517
DB 408 GCTTCTCTCAACCAAGTAGAGATGAGCTGTTCTGAACCTTGTATGAGTATGTCC 467
QY 518 CTGAGACTTTTACCGGTTTGGGCACTACTACTGTTCTTAATCAGAGGATGCCAAATTT 577
DB 468 CGGAGCGCTATACCGGCTGTTAGGCACTACAGTAAATGCCAACCGGGATGCCGCTTA 527
QY 578 TCTATGTCAAGCTTTACATATCAATATCTTTAGAGGTTTGGCTTTACATCCATCTGTTTC 637
DB 528 TCTATGTCAAGCTTTACATATCAAGCTTTTAGAGGCTAGCTTATGTTCTCATCTGTTTC 587
QY 638 CCGGTGTTTGCACAGAGATGTGAACCAACCAAAATCTCTTGGTTCATCCCTTGACCCATC 697
DB 588 CAGGAGTTTGCACAGGAGTGTGAACCAACCAAAATGTTTGGTTCATCTCTTAACCCATC 647
QY 698 AGTTAAAGCTGTGATTTTGAAGTGTGAAGTATGTTGTCAAAGTGAACCAACATAT 757
DB 648 AAGTCAGATCTGAGCTTTGGAAGTGTGAAGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTT 707
QY 758 CATATATCTGCTCCGTTATTAATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 817
DB 708 CATATATCTGCTCCGTTATTAATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 767
QY 818 CAGCATCATAGATATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 877
DB 768 CAACCTTCAATAGACATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 827
QY 878 CGTTATTTCCAGGAGAAATTCAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 937
DB 828 CTCTGTTTCCAGGAGAGACTGCGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 887
QY 938 CTCCAACTCGTGAAGAAATTCAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 997
DB 888 CTCCAACTCGTGAAGAAATTCAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 947
QY 998 AAATCAAGCTCACCTTTGGCAAGAGTTTTCATAAAGCGATGCTTCCAGAGCAATAG 1057
DB 948 AGATTAAGGCTCATCTTTGGCAAGAGTTTTCATAAAGCGATGCTTCCAGAGCAATAG 1007
QY 1058 ACCTTGCACTCTGGCTTCTTCAATATTCACCAAGTCTACGCTGCACTGGCTCGAGCAT 1117
DB 1008 ATCTTGGCTTCCGCTTCTTCCAGTATTCACCAATCTACGTTGCACTGCTCTTGAATGAT 1067
QY 1118 GTGCTCATCTCGGTTTTCATGAATCTCCAGAGCCCAAGCGCGCTCTTCCAAATGCTCGTC 1177
DB 1068 GTGCACTATCTCTTCTTGTAGTACGTTGAGCCGATGACGCTTGCAGATGCGCGCC 1127
QY 1178 CATTACCGCCATTTGTTCAATTTCAAAACAAGAGTTAGGTGAGCTTCAATGGAGCTAATCA 1237

DB 1128 CATTCCCTCTCTCTGTTCAACTTCAAACTGAACTAGCGAAGCGCTTCTCCAGAGCTCATCA 1187
QY 1238 ACAGGCTAATACCTGAGCATGTGAGACGACAAATGAGCAC 1277
DB 1188 ACAGGCTTGTTCGCGAACATGTTGACGCGCAAAATGGGCC 1227
RESULT 12
AAC41916
ID AAC41916 standard; DNA; 1635 BP.
XX
AC AAC41916;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 33613.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
FN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-00301439.
XX
PR 25-FEB-1999; 99US-0121825P.
PR 05-MAR-1999; 99US-0123180P.
PR 09-MAR-1999; 99US-0123548P.
PR 23-MAR-1999; 99US-0125788P.
PR 25-MAR-1999; 99US-0126264P.
PR 29-MAR-1999; 99US-0126785P.
PR 01-APR-1999; 99US-0127462P.
PR 06-APR-1999; 99US-0128234P.
PR 08-APR-1999; 99US-0128714P.
PR 16-APR-1999; 99US-0129845P.
PR 19-APR-1999; 99US-0130077P.
PR 21-APR-1999; 99US-0130449P.
PR 23-APR-1999; 99US-0130510P.
PR 23-APR-1999; 99US-0130891P.
PR 28-APR-1999; 99US-0131449P.
PR 30-APR-1999; 99US-0132048P.
PR 30-APR-1999; 99US-0132407P.
PR 04-MAY-1999; 99US-0132484P.
PR 05-MAY-1999; 99US-0132485P.
PR 06-MAY-1999; 99US-0132486P.
PR 07-MAY-1999; 99US-0132487P.
PR 11-MAY-1999; 99US-0132566P.
PR 14-MAY-1999; 99US-0134218P.
PR 14-MAY-1999; 99US-0134219P.
PR 14-MAY-1999; 99US-0134221P.
PR 18-MAY-1999; 99US-0134370P.
PR 19-MAY-1999; 99US-0134768P.
PR 20-MAY-1999; 99US-0134941P.
PR 21-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136021P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.

PR	16-JUN-1999;	99US-0139452P.	PR	12-AUG-1999;	99US-0148341P.
PR	16-JUN-1999;	99US-0139453P.	PR	13-AUG-1999;	99US-0148565P.
PR	17-JUN-1999;	99US-0139492P.	PR	13-AUG-1999;	99US-0148684P.
PR	18-JUN-1999;	99US-0139454P.	PR	16-AUG-1999;	99US-0149368P.
PR	18-JUN-1999;	99US-0139455P.	PR	17-AUG-1999;	99US-0149175P.
PR	18-JUN-1999;	99US-0139456P.	PR	18-AUG-1999;	99US-0149426P.
PR	18-JUN-1999;	99US-0139457P.	PR	20-AUG-1999;	99US-0149722P.
PR	18-JUN-1999;	99US-0139458P.	PR	20-AUG-1999;	99US-0149723P.
PR	18-JUN-1999;	99US-0139459P.	PR	20-AUG-1999;	99US-0149929P.
PR	18-JUN-1999;	99US-0139460P.	PR	23-AUG-1999;	99US-0149902P.
PR	18-JUN-1999;	99US-0139461P.	PR	23-AUG-1999;	99US-0149930P.
PR	18-JUN-1999;	99US-0139462P.	PR	25-AUG-1999;	99US-0150566P.
PR	18-JUN-1999;	99US-0139463P.	PR	26-AUG-1999;	99US-0150884P.
PR	18-JUN-1999;	99US-0139750P.	PR	27-AUG-1999;	99US-0151065P.
PR	18-JUN-1999;	99US-0139763P.	PR	27-AUG-1999;	99US-0151066P.
PR	21-JUN-1999;	99US-0139817P.	PR	27-AUG-1999;	99US-0151080P.
PR	22-JUN-1999;	99US-0139899P.	PR	30-AUG-1999;	99US-0151303P.
PR	23-JUN-1999;	99US-0140353P.	PR	31-AUG-1999;	99US-0151438P.
PR	24-JUN-1999;	99US-0140354P.	PR	07-SEP-1999;	99US-0151930P.
PR	24-JUN-1999;	99US-0140695P.	PR	07-SEP-1999;	99US-0152363P.
PR	28-JUN-1999;	99US-0140823P.	PR	10-SEP-1999;	99US-0153070P.
PR	29-JUN-1999;	99US-0140991P.	PR	13-SEP-1999;	99US-0153758P.
PR	30-JUN-1999;	99US-0141287P.	PR	15-SEP-1999;	99US-0154018P.
PR	01-JUL-1999;	99US-0141842P.	PR	16-SEP-1999;	99US-0154039P.
PR	01-JUL-1999;	99US-0142154P.	PR	20-SEP-1999;	99US-0154779P.
PR	02-JUL-1999;	99US-0142055P.	PR	22-SEP-1999;	99US-0155139P.
PR	06-JUL-1999;	99US-0142390P.	PR	23-SEP-1999;	99US-0155486P.
PR	08-JUL-1999;	99US-0142803P.	PR	24-SEP-1999;	99US-0155659P.
PR	09-JUL-1999;	99US-0142920P.	PR	28-SEP-1999;	99US-0156458P.
PR	12-JUL-1999;	99US-0142977P.	PR	29-SEP-1999;	99US-0156596P.
PR	13-JUL-1999;	99US-0143342P.	PR	04-OCT-1999;	99US-0157117P.
PR	14-JUL-1999;	99US-0143624P.	PR	05-OCT-1999;	99US-0157753P.
PR	15-JUL-1999;	99US-0144005P.	PR	06-OCT-1999;	99US-0157865P.
PR	16-JUL-1999;	99US-0144085P.	PR	07-OCT-1999;	99US-0158029P.
PR	16-JUL-1999;	99US-0144086P.	PR	08-OCT-1999;	99US-0158232P.
PR	19-JUL-1999;	99US-0144325P.	PR	12-OCT-1999;	99US-0158369P.
PR	19-JUL-1999;	99US-0144331P.	PR	13-OCT-1999;	99US-0159293P.
PR	19-JUL-1999;	99US-0144332P.	PR	13-OCT-1999;	99US-0159294P.
PR	19-JUL-1999;	99US-0144333P.	PR	13-OCT-1999;	99US-0159295P.
PR	19-JUL-1999;	99US-0144334P.	PR	14-OCT-1999;	99US-0159329P.
PR	19-JUL-1999;	99US-0144335P.	PR	14-OCT-1999;	99US-0159330P.
PR	20-JUL-1999;	99US-0144352P.	PR	14-OCT-1999;	99US-0159331P.
PR	20-JUL-1999;	99US-0144632P.	PR	14-OCT-1999;	99US-0159637P.
PR	20-JUL-1999;	99US-0144684P.	PR	14-OCT-1999;	99US-0159638P.
PR	21-JUL-1999;	99US-0144814P.	PR	18-OCT-1999;	99US-0159584P.
PR	21-JUL-1999;	99US-0145086P.	PR	21-OCT-1999;	99US-0160741P.
PR	21-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160767P.
PR	22-JUL-1999;	99US-0145087P.	PR	21-OCT-1999;	99US-0160768P.
PR	22-JUL-1999;	99US-0145088P.	PR	21-OCT-1999;	99US-0160770P.
PR	22-JUL-1999;	99US-0145089P.	PR	21-OCT-1999;	99US-0160814P.
PR	22-JUL-1999;	99US-0145192P.	PR	21-OCT-1999;	99US-0160815P.
PR	23-JUL-1999;	99US-0145145P.	PR	22-OCT-1999;	99US-0160980P.
PR	23-JUL-1999;	99US-0145218P.	PR	22-OCT-1999;	99US-0160981P.
PR	23-JUL-1999;	99US-0145224P.	PR	22-OCT-1999;	99US-0160989P.
PR	26-JUL-1999;	99US-0145276P.	PR	25-OCT-1999;	99US-0161404P.
PR	27-JUL-1999;	99US-0145913P.	PR	25-OCT-1999;	99US-0161405P.
PR	27-JUL-1999;	99US-0145918P.	PR	25-OCT-1999;	99US-0161406P.
PR	27-JUL-1999;	99US-0145519P.	PR	26-OCT-1999;	99US-0161359P.
PR	28-JUL-1999;	99US-0145951P.	PR	26-OCT-1999;	99US-0161360P.
PR	02-AUG-1999;	99US-0146386P.	PR	26-OCT-1999;	99US-0161361P.
PR	02-AUG-1999;	99US-0146388P.	PR	28-OCT-1999;	99US-0161920P.
PR	02-AUG-1999;	99US-0146389P.	PR	28-OCT-1999;	99US-0161992P.
PR	03-AUG-1999;	99US-0147038P.	PR	28-OCT-1999;	99US-0161993P.
PR	04-AUG-1999;	99US-0147204P.	PR	29-OCT-1999;	99US-0162142P.
PR	04-AUG-1999;	99US-0147302P.			
PR	05-AUG-1999;	99US-0147192P.			
PR	05-AUG-1999;	99US-0147260P.			
PR	06-AUG-1999;	99US-0147303P.			
PR	06-AUG-1999;	99US-0147416P.			
PR	08-AUG-1999;	99US-0147493P.			
PR	09-AUG-1999;	99US-0147935P.			
PR	10-AUG-1999;	99US-0148171P.			
PR	11-AUG-1999;	99US-0148319P.			

Query Match 43.3%; Score 698.4; DB 3; Length 1635;
 Best Local Similarity 77.1%; Pred. NO. 4.3e-178;
 Matches 863; Conservative 0; Mismatches 256; Indels 1; Gaps 1;
 QY 164 TGGATTCTGATAAGGAATGCTGCAGCTGTTATTCAGGGAATGACGCTGTACTGGTC 223
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 DB 174 TGGCTGATGATAAGGAGATGCCTGCTGTAGTGTGATGACATGATCAAGTCACTGGTC 233
 |||||

QY 224 ATATCATTTCCACTACTATAGGAGCAAAACCGCGAACCAAGCAGACCATTTAGTTACA 283
 Db |||||
 QY 234 ATATTTATTTCCACCAATCGTGGGCAAAATGGTGAACCAAAACAGAAATAGTTACA 293
 Db |||||
 QY 284 TGGCTGAGCGGTTGTGGAAACAGGTTTCATTTCGGGATTTTTCAGGCGAAATGCTTGG 343
 Db |||||
 QY 294 TGGCGGA-CGAGTTGTGGTACAGGCTCGTTTCGGGATCGTTTTCAGCAAAATGTTGG 352
 Db |||||
 QY 344 AAACCTGGAGAAATCAGTAGCCATTAAGAGTCTTGCAGAGATCGAGCTATATAAAACCGTG 403
 Db |||||
 QY 353 AGACTGGAGAAACCGTGGCGATAAAGAGGTTTTCAGAGATAGAAGATCAAGAACCGAG 412
 Db |||||
 QY 404 AGTTGCAACTATGTCGACCAAGTATGATCCCAAAATGTCATCTCTTGAAGCACTGTTCT 463
 Db |||||
 QY 413 AACTTCAGTTGATGCGTGTGATGGATATCCGAATGTGGTTTGTGGAAGCAATGCTTCT 472
 Db |||||
 QY 464 TCTCTACACAGTAGATAGAGTCTTCTCTCAACCTTGTATGAGTATGTACCTGAGA 523
 Db |||||
 QY 473 TTTTCGACTACAGTAAAGAGAGCTTTTCTTGAACCTTGTGATGAGTATGTCCCTGAGA 532
 Db |||||
 QY 524 CTTTATACCGGTTTGGGCACTATACATAGTCTTAAATCAGAGGATGCCAATTTTCTATG 583
 Db |||||
 QY 533 GCTTGTATCGAGTTCTGAAACATATAGTAGTGCACAAACCAAGAAATGCTCTTGTCTATG 592
 Db |||||
 QY 584 TCAAGCTTTACACATATCAAACTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGGTG 643
 Db |||||
 QY 593 TTAACCTTTACATGATCAGATCTTCCGGGGACITGCTTTACATTCACAAATGTTGTGAG 652
 Db |||||
 QY 644 TTTGCGACAGAGATGTGAACACCAAAATCTCTGTTGATCCCTTGACCCATCAGGTTA 703
 Db |||||
 QY 653 TTTGTCACAGAGATCTAAGCCTCAAAATCTTCTGTTGATCTTCTTACTCATCAAGTCA 712
 Db |||||
 QY 704 AGCTGTGTATTTGGAAGTGCAGAAATGTTGGTCAAAAGGTGAACCAACATATCATATA 763
 Db |||||
 QY 713 AAATCTGTGACTTTGGCAGTGCAGAACAGCTCGTTAAAGGTGAAGCAACATTTCTTACA 772
 Db |||||
 QY 764 TCTGCTCCGTTATTTATGCTGCTCAGAACTCATCTTTGGCGCCACAGAGTATACAGAT 823
 Db |||||
 QY 773 TCTGCTCAGATTTACCGTGACCGGAGCTCATATTTGGTCCACTGAGTACACAACT 832
 Db |||||
 QY 824 CCATAGATATATGCTGCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 883
 Db |||||
 QY 833 CTATTTGATATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 892
 Db |||||
 QY 884 TTCCAGGAGAAATTCAGTTGATCAGCTTTGGAGATCATAAAGTTCTTGGTACTCCAA 943
 Db |||||
 QY 893 TTCCCGGAGAAATTCAGTTGATCAGCTTTGGAGATCATAAAGTTCTTGGTACTCCAA 952
 Db |||||
 QY 944 CTCGTGAAGAAATTCAGTTGATGAAACCGAATCAGAGATTTTGGTTCACCAAAATCA 1003
 Db |||||
 QY 953 CTCGAGAGAAATTCAGTTGATGAAATCCACATTCACAGATTTTGGTTCACAGATAA 1012
 Db |||||
 QY 1004 AAGCTCACCTTTGGCACAAGGTTTTCATAAACGATGCTCCAGAACCAATAGACCTTG 1063
 Db |||||
 QY 1013 AGGCAATCTCTGGCACAAGATCTTCCACAAAGATGCCCCAGAGGATGATTTG 1072
 Db |||||
 QY 1064 CATCTCGGCTTCTCAATATTCACCAAGTCTACGCTGCACTGCGTTCGAAGCATGTGCTC 1123
 Db |||||
 QY 1073 CATCAAGCTGCTTCAATATCTTCCAGTCTAAGATGCACAGCGCTCGAGCTTGTGCAC 1132
 Db |||||
 QY 1124 ATCCGTTTTTCAATGAACTCCGAGAGCCAAACCGCGCTTCCAAATGGTGTCTCAATAC 1183
 Db |||||
 QY 1133 ATCCGTTTTTCAATGAACTCCGAGAGCCAAACCGCTGCTTTCACAAATGGAGCGCTTTC 1192
 Db |||||
 QY 1184 CGCCATTTGTTCAATTTCAACAGAGTTAGTGGAGCTTCAATGAGCTTAATCAACAGCG 1243
 Db |||||
 QY 1193 CGCCTTCTTCAATTTCAACAGAGTTAGTGGAGCTTCAATGAGCTTAATCAACAGCG 1252
 Db |||||
 QY 1244 TAATACCTGAGCATGTGAGACGCAAAATGAGCAGAGGAT 1283
 Db |||||
 QY 1253 TGATTTCCAGACCATATCAGAGACAAATTTGGTCTAAGCTT 1292
 Db |||||

RESULT 13
 ACC57973
 ID ACC57973 standard; cDNA; 1499 BP.
 XX
 AC ACC57973;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Soybean protein kinase stress-related polypeptide GmpK-1 cDNA.
 XX
 KW GmpK-1; protein kinase stress-related polypeptide; PKSRP; enzyme;
 XX transgenic plant; plant; stress tolerance; drought tolerance;
 KW salt tolerance; cold tolerance; soybean; gene; ss.
 XX
 OS Glycine max.
 XX
 FH Key Location/Qualifiers
 CDS 53..1282
 FT /*tag= a
 FT /product= "GmpK-1"
 XX
 PN WO2003040171-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 12-NOV-2002; 2002WO-US036374.
 XX
 PR 09-NOV-2001; 2001US-0346096P.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Van Thiel N, Da Costa E SilvaO, Chen R;
 XX
 DR WPI; 2003-441522/41.
 DR P-PSDB; ABR42366.
 XX
 PT New protein kinase stress-related polypeptide coding nucleic acid, useful
 PT for producing transgenic plants with an increased tolerance to an
 PT environmental stress, e.g. high salinity, as compared to a wild type
 PT variety of the plant.
 XX
 PS Claim 1; Page 94-95; 111pp; English.
 CC
 CC The present sequence is a full-length cDNA encoding GmpK-1, a novel
 CC soybean protein kinase stress-related polypeptide (PKSRP). The cDNA was
 CC identified on the basis of homology to Physcomitrella patens PK-3 (see
 CC ACC57962) and PK-10 (see ACC57966) sequence. GmpK-1 is an example of
 CC PKSRPs of the invention that are important for modulating a plant's
 CC response to environmental stress. Over-expression of PKSRP coding nucleic
 CC acids in a plant results in the plant's increased tolerance to
 CC environmental stress. Transgenic monocot and dicot plants are provided
 CC that show increased tolerance to high salinity, drought and low
 CC temperature
 XX
 SQ Sequence 1499 BP; 431 A; 335 C; 336 G; 397 T; 0 U; 0 Other;
 Query Match 43.0%; Score 693.4; DB 8; Length 1499;
 Best Local Similarity 76.2%; Pred. No. 9.3e-177;
 Matches 853; Conservative 0; Mismatches 266; Indels 0; Gaps 0;
 QY 152 GCGGCTCCGATGTTGATTTCTGATAGGAATGTCGACGCTGTTATGAGGAAATGACG 211
 Db |||||
 QY 153 GCGGCTCCGACGCGCGCACCGAAAGGAAATGTCAGCTCTCTGTCAGATGTAATGATG 212
 Db |||||
 QY 212 CTGTTACTGTCATATCTTCCACTACTATAGGAGGCAAAACCGCAACCAAGCAGA 271
 Db |||||
 QY 213 CACTCAGCTGGTTCATAATCTCAACCAATTCAGGAGCAAAATGCGCAACCTAAACAA 272
 Db |||||
 QY 272 CCATTAGTTACATGCTGAGCGGTTGTTGGAAACAGGTTTCATTTCGGGATTTGTTTTCAGG 331
 Db |||||
 QY 273 CCATCAGTTACATGCGCAACGTTGTTGGCACTGGATCATTTGGCATTGTTTCCAGG 332
 Db |||||
 QY 332 CGAAATGCTTGGAAACTCGAGAAATCAGTAGCAATTAAGGCTTTGCAAGATCGACGCT 391
 Db |||||

Db 333 CGAAGTCTTGAGACTGCGGAGGAGTGGCTATAAAGAGTCTTGCAGGACAGGCGAT 392
 Qy 392 ATAAACCGTGTGAGTGAACCTAATCGACCATGATGATCACCCTAATGCTCTCTTGA 451
 Db 393 ACAAACCTGTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 452
 Qy 452 AGCAGTCTTCTCTCTACAAAGAGTGTGATGATGATGATGATGATGATGATGATGAT 511
 Db 453 GTAACCTATCTCTCTACAAAGAGTGTGATGATGATGATGATGATGATGATGATGAT 512
 Qy 512 ATGTACCTGAGCTTTATACCGGTTTTCAGGCACTATCTAGTCTTCTAATCAGAGGATCC 571
 Db 513 ATGTCTCTGAGGATCTTCCGTTTATAAGCACTACAGTGTGATGATGATGATGATGAT 572
 Qy 572 CAATTTCTATGTCAAGCTTTACACATATCAATCTTTAGAGGTTTGGCTTACATCCATA 631
 Db 573 CCTAATCTATGTGAATTTATATACATATCAATCTTTAGGAGCTTGGCTTATCCATA 632
 Qy 632 CTGTTCCCGTGTTCGCCACAGATGTGAACCAAAATCTCTTGGTTGATCCCTGA 691
 Db 633 CTGTACAGGAATCTGCCATAGGAATTTGAGGCTCAAAATCTTTTGGTTGATCGACTCA 692
 Qy 692 CCCATCAGGTTAAGCTGTGTGATTTTGGAAAGTCAAAAGTATTTGGTCAAAAGTGAACCA 751
 Db 693 CACCAAGTCAAGCTCTGTGATTTTGGAGTGCAGAAAGTCTGTGTGGAGGTGAATCAA 752
 Qy 752 ACATATCATATCTCTCTCGTATATATCGTCTCAGAACTCATCTTTGGGCGCACAG 811
 Db 753 ACATTTTATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 812
 Qy 812 AGTATACAGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 871
 Db 813 ATACACAACTCTGTGTGATTTTGGTTCGCTGTGTGTCTTGGGAACTTCTCTAG 872
 Qy 872 GCAGCGCTTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTTC 931
 Db 873 GCCAGCTTTGTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTTC 932
 Qy 932 TTGGTACTCAACTCTGTGAAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTTC 991
 Db 933 TTGGTACTCTACTCGAGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTTC 992
 Qy 992 TCCCAAAATCAAGCTCAAGCTTGTGAGCAAGGTTTTCATAAAGGATGCTTCCAGAAAG 1051
 Db 993 TCCCAAAATCAAGCTCAAGCTTGTGAGCAAGGTTTTCATAAAGGATGCTTCCAGAAAG 1052
 Qy 1052 CAATAGACCTTGCATCTCGGCTTCTTCAATATTCACCAAGTCTACGCTGCAGCTCGCTCG 1111
 Db 1053 CAATAGACCTTGCATCAAGGCTTCTTCAATATTCACCAAGTCTACGCTGCAGCTCGCTCG 1112
 Qy 1112 AAGCATGTCTCATCTCGTCTTCAATATTCACCAAGTCTACGCTGCAGCTCGCTCGCTCG 1171
 Db 1113 AAGCAATGGCAGATCTCTTCTTGGAGAGCTTCCGAGGAGCTTCCGAGGAGCTTCCGAGG 1172
 Qy 1172 GTCTGCTTACCTGCTTCTTCAATATTCACCAAGTCTACGCTGCAGCTCGCTCGCTCG 1231
 Db 1173 GTCTGCTTACCTGCTTCTTCAATATTCACCAAGTCTACGCTGCAGCTCGCTCGCTCG 1232
 Qy 1232 TAATCAACAGGCTTAATCTTCAATATTCACCAAGTCTACGCTGCAGCTCGCTCGCTCG 1270
 Db 1233 TGCTTCTTAAGCTCATCCAGAGCATGTGAGGCGGCAAA 1271

RESULT 14

ACC57970

ID ACC57970 standard; cDNA; 1621 BP.

XX ACC57970;

AC ACC57970;

XX 11-AUG-2003 (first entry)

DE Canola protein kinase stress-related polypeptide BnPK-2 cDNA.

XX BnPK-2; protein kinase stress-related polypeptide; PKSRP; enzyme;
 KW transgenic plant; plant; stress tolerance; drought tolerance;
 KW salt tolerance; cold tolerance; canola; gene; ss.
 OS Brassica napus.
 XX Key Location/Qualifiers
 FT CDS 132..1277
 FT /*tag= a
 FT /product= "BnPK-2"
 XX WO2003040171-A2.
 XX 15-MAY-2003.
 XX 12-NOV-2002; 2002WO-US036374.
 XX 09-NOV-2001; 2001US-0346096P.
 XX (BADI) BASF PLANT SCI GMBH.
 XX Van Thiel N, Da Costa E SilvaO, Chen R;
 XX WPI; 2003-441522/41.
 XX P-PSDB; ABR42363.
 XX New protein kinase stress-related polypeptide coding nucleic acid, useful
 PT for producing transgenic plants with an increased tolerance to an
 PT environmental stress, e.g. high salinity, as compared to a wild type
 PT variety of the plant.
 XX Claim 1; Page 90-91; 111pp; English.
 CC The present sequence is a full-length cDNA encoding BnPK-2, a novel
 CC canola protein kinase stress-related polypeptide (PKSRP). The cDNA was
 CC identified on the basis of homology to Physcomitrella patens PK-3 (see
 CC ACC57962) and PK-10 (see ACC57966) sequence. BnPK-2 is an example of
 CC PKSRPs of the invention that are important for modulating a plant's
 CC response to environmental stress. Over-expression of PKSRP coding nucleic
 CC acids in a plant results in the plant's increased tolerance to
 CC environmental stress. Transgenic monocot and dicot plants are provided
 CC that show increased tolerance to high salinity, drought and low
 CC temperature
 XX Sequence 1621 BP; 450 A; 371 C; 331 G; 469 T; 0 U; 0 Other;
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 Best Local Similarity 74.5%; Pred. No. 8.6e-173;
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KW protein identification; signal transduction pathway; metabolic; pathway;
KW promoter; termination sequence; corn; ss.
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US-09-347-801-15
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 ; Patent No. 6262345
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 ; APPLICANT: Allen, Steve
 ; APPLICANT: Lee, Jian Ming
 ; TITLE OF INVENTION: Plant Protein Kinases
 ; FILE REFERENCE: BB-1171
 ; CURRENT APPLICATION NUMBER: US/09/347,801
 ; CURRENT FILING DATE: 1999-07-02
 ; EARLIER APPLICATION NUMBER: 60/092,438
 ; EARLIER FILING DATE: July 10, 1998
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 15
 ; LENGTH: 1673
 ; TYPE: DNA
 ; ORGANISM: Triticum aestivum
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1349)
 ; US-09-347-801-15

Query Match 43.5%; Score 701.6; DB 3; Length 1673;
 Best Local Similarity 74.7%; Pred. No. 3.5e-200;
 Matches 881; Conservative 0; Mismatches 299; Indels 0; Gaps 0;

98 AGCCTCATGCTCTGCTCGCGCTGCGAGCTTCAAGACGCGAGCGCTTTGAAACGCGGTC 157
 48 AGCATCCGCGCGCGCGCGAGCCGATGCTGCTCGACGAGCGCCCCACCGCAGTCG 107
 158 CTGAATTGATTCTGTATAGGAAATGCTCTGACGCTGTTATTGAGGGAATGACGCTGTTA 217
 108 CTGCGAAGAAAGACAGCAGGATGGCGAGCGCGGCTATCGGAGGGAGACGACCCATGA 167
 218 CTGGTCATATCATTTTCCACTACTATAGGAGGCAAAACCGCGAACCAAGCAGACCATTA 277
 168 CCGGTCACATCATCTCCACCACCATCGCGGCAAGAACCGAGCGCAAGCAGCATTA 227
 278 GTTACATGCTGAGCGGGTTGTTGNAACAGGTTTCATTCGGGATTTGTTTCAGGCGGAAT 337
 228 GCTACATGCGGAGCGCGTGTGTGGGCACTGGTTGCTTTGGCATCGCTTTTCAGGCTAAAT 287


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QY 338 GCTTGGAACTGGAGATCAGTAGCATTAATTAAGGCTCTTGCAGATCGAGCTATATAA 397
Db 288 GCCTGGAAACCGGGGAGATGGTGGCATTAAGAGGCTACTGCAGGACGAGCGTACAAGA 347
QY 398 ACCGTGAGTTGCAACTAATATCGACCAATAGATGATGATGATGATGATGATGATGAT 457
Db 348 ACCGTGAGTTGCAACTAATATCGACCAATAGATGATGATGATGATGATGATGATGAT 407
QY 458 GTTCTCTCTCTCAACAGAGTAGAGATGATGATGATGATGATGATGATGATGATGATGAT 517
Db 408 GCTTCTCTCTCAACAGAGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 467
QY 518 CTGAGACTTTATACCGGCTTTGAGGCACTATAGTCTTCTCAACCTTCTTATGAGAGTATGAT 577
Db 468 CGGAGACGCTATACCGGCTTTGAGGCACTATAGTCTTCTCAACCTTCTTATGAGAGTATGAT 527
QY 578 TCTATGTCAGGCTTTATACATATCAATCTTTAGAGGCTTTGAGGCTTTATGAGGCTTTATGAG 637
Db 528 TCTATGTCAGGCTTTATACATATCAATCTTTAGAGGCTTTGAGGCTTTATGAGGCTTTATGAG 587
QY 638 CCGGTGTTTGGCACAGAGATGTGAACCAACCAAAATCTCTTGGTGTGATCCCTTGAACCCATC 697
Db 588 CAGGAGTTTGGCACAGGAGTGTGAACCAACCAAAATGTTTGGTGTGATCCCTTGAACCCATC 647
QY 698 AGTTAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 757
Db 648 AAGTCAAGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 707
QY 758 CATATATCTGCTCCGCTTTATATCTGCTCCAGAACTCATCTTTGCGGCCACAGAGTATA 817
Db 708 CATACATATGCTCTCGCTACTATCTGCTCTGAGCTCATATTTGGTGGAACTGAAATATA 767
QY 818 CAGCATTCATAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 877
Db 768 CAACCTTCAATAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 827
QY 878 GCTTATTTCCAGGAGAAATTCAGTTGATGATGATGATGATGATGATGATGATGATGATGAT 937
Db 828 CTCGTGTTTCCAGGAGAGATGCGGTTGATGATGATGATGATGATGATGATGATGATGATGAT 887
QY 938 CTCCAACTCGTGAACAAATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 997
Db 888 CTCCAACTCGTGAACAAATTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 947
QY 998 AAATCAAGCTCACCTTGGCAAGAGTTTTCATAAAGGATGCTCCAGAGCAATAG 1057
Db 948 AGATTAAGCTCATCTTGGCACAGATTTTCCACAGAGATGCGCGCTGAGCTATAG 1007
QY 1058 ACCTTGCACTCGGCTTCTTCAATATTCACCAAGTCTAGCTGCACTGCGCTCGAAGCAT 1117
Db 1008 ATCTTGGCCTCCGCTTCTTCAAGTATTCACCAAAATCTAGCTGCACTGCTCTTGAATGCA 1067
QY 1118 GTGCTCATCGGCTTTTCAATGAACTCCGAGAGCCAAACGCGCTCTTCCAATGCTGCTC 1177
Db 1068 GTGCAATCTCTTCTTGAAGTACGCTGAGCCGAATGCACTGCTTGGCAATGCGGCC 1127
QY 1178 CATTAACCGCATTTGTTCAATTTCAAAACAGAGTTAGTGGAGCTTCAATGAGAGCTAATCA 1237
Db 1128 CATTCCTCTCTGTTCAATCTTCAACCTGAACTAGCGAAGCGCTCTCCAGAGCTCATCA 1187
QY 1238 ACAGGCTAATACCTGAGCATGTGAGACGACAAATGAGCAC 1277
Db 1188 ACAGGCTTGTTCGGAACATGTTTCGACGCAAAATGGGCC 1227

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RESULT 3

US-09-854-731-15
 ; Sequence 15, Application US/09854731
 ; Patent No. 6794561
 ; GENERAL INFORMATION:
 ; APPLICANT: Allen, Steve
 ; APPLICANT: Lee, Jian Ming
 ; TITLE OF INVENTION: Plant Protein Kinases

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; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 15
; LENGTH: 1673
; TYPE: DNA
; ORGANISM: Triticum aestivum
; NAME/KEY: unsure
; LOCATION: (1349)
; US-09-854-731-15

Query Match 43.5%; Score 701.6; DB 4; Length 1673;
Best Local Similarity 74.7%; Pred. No. 3.5e-200;
Matches 881; Conservative 0; Mismatches 299; Indels 0; Gaps 0;

QY 98 AGCCTCATGCTCTTCTCCGCGCTGACGCTTCAAGCGGCGAGCGCTTTTGAACCCGCTC 157
Db 48 AGCATCCGCGCGCGCGCGCGCGCGATGCTGCTCGACGAGCAGCCGCCACCGCAGTCG 107
QY 158 CTGAATGGATCTTGATGAAGAAATGCTGACGCTGTTTATTTGAGGGAATGACGCTGTTA 217
Db 108 CTGCGAAGAAGCAGCAGGATGCGGAGCGCGCGTATGCGGAGGGGAACGACGCCATGA 167
QY 218 CTGGTCATATCATTTCCACTACTATAGGAGCAAAACCGGCAACCAAGAGAGACATTA 277
Db 168 CCGTCCATCATCTCCACACCATCGCGCGCAAGAGCGGCGGCGGCGGCGGCGGCGGCGG 227
QY 278 GTTACATGGCTGAGCGGCTTGTGGAACAGAGTTCAATCGGGAATGTTTTTCAGGCGAAT 337
Db 228 GCTACATGGCGGAGCGCGCTTGTGGGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 287
QY 338 GCTTGGAACTGGAGATCAGTAGCATTAATTAAGGCTCTTGCAGATCGAGCTATATAA 397
Db 288 GCCTGGAAACCGGGGAGATGGTGGGCACTTAAGAGGCTACTGCAGGACGAGCGGTACAAGA 347
QY 398 ACCGTGAGTTGCAACTAATATCGACCAATAGATGATGATGATGATGATGATGATGATGAT 457
Db 348 ACCGTGAGTTGCAACTAATATCGACCAATAGATGATGATGATGATGATGATGATGATGAT 407
QY 458 GTTCTCTCTCTCAACAGAGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 517
Db 408 GCTTCTCTCTCAACAGAGTAGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 467
QY 518 CTGAGACTTTATACCGGCTTTGAGGCACTATAGTCTTCTCAACCTTCTTATGAGAGTATGAT 577
Db 468 CGGAGACGCTATACCGGCTTTGAGGCACTATAGTCTTCTCAACCTTCTTATGAGAGTATGAT 527
QY 578 TCTATGTCAGGCTTTATACATATCAATCTTTAGAGGCTTTGAGGCTTTATGAGGCTTTATGAG 637
Db 528 TCTATGTCAGGCTTTATACATATCAATCTTTAGAGGCTTTGAGGCTTTATGAGGCTTTATGAG 587
QY 638 CCGGTGTTTGGCACAGAGATGTGAACCAACCAAAATCTCTTGGTGTGATCCCTTGAACCCATC 697
Db 588 CAGGAGTTTGGCACAGGAGTGTGAACCAACCAAAATGTTTGGTGTGATCCCTTGAACCCATC 647
QY 698 AGTTAAGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 757
Db 648 AAGTCAAGATCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 707
QY 758 CATATATCTGCTCCGCTTTATATCTGCTCCAGAACTCATCTTTGCGGCCACAGAGTATA 817
Db 708 CATACATATGCTCTCGCTACTATCTGCTCTGAGCTCATATTTGGTGGAACTGAAATATA 767
QY 818 CAGCATTCATAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 877
Db 768 CAACCTTCAATAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 827
QY 878 GCTTATTTCCAGGAGAAATTCAGTTGATGATGATGATGATGATGATGATGATGATGATGAT 937

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Db 828 CTCTGTTCCAGGAGAGACTGCGGTTGATCAGCTAGTGGAGATTATCAAGGTTCTTGGTA 887
QY 938 CTCCTCACTCGTGAAGAAATTCGATGATGAACCCGAACTACACAGATTTTGGTCCCAAC 997
Db 888 CTCCTCACTCGTGAAGAAATTCGATGATGAACCCGAACTATACCGAGTTTCAGGTTTCCTC 947
QY 998 AAATCAAGCTCACCCCTCGGCACAAGGTTTTTCAAAACGATGCTCCAGAGCAATAG 1057
Db 948 AGATTAAGGCTCATCTCTGGCACAAGATTTTCAACGAAGATGCGCGTGAAGCTATAG 1007
QY 1058 ACCTTGATCTCGGCTCTTCAATATTCACCAAGTCTACGCTGCACTGCGCTCGAAGCAT 1117
Db 1008 ATCTTGCTCCCGCTCTTCCAGTATTCACCAATCTACGTTGCACTGCTCTTGATGCAT 1067
QY 1118 GTGCTCATCGGTTTTCAATGAAGTCTCGAGAGCCGAAACCGCTCTTCAAAATGTCGTC 1177
Db 1068 GTGCAATCTCTCTTTGTAGAGTACGTTGAGCCGAATGACGCTTGGCGAATGGCGGC 1127
QY 1178 CATTACCGCATGTTTCAATTTCAAAACAGAGTTAGGTGGAGCTTCAATGGAGCTAATCA 1237
Db 1128 CATTCCTCTCTGTTCACTTCAAACTTGAACCTGAACTAGCGAAGGCTCTCCAGAGCTCATCA 1187
QY 1238 ACAGGCTAATACCTGAGCATGTGAGACGACAAATGAGCAC 1277
Db 1188 ACAGGCTTGTTCGGAAACATGTTTCGACGGCAAAATGGCCC 1227

RESULT 4

US-09-347-801-9
; Sequence 9, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; EARLIER FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1814
; TYPE: DNA
; ORGANISM: Zea mays
US-09-347-801-9

Query Match 34.1%; Score 549.8; DB 3; Length 1814;
Best Local Similarity 70.8%; Pred. No. 1.6e-154;
Matches 731; Conservative 0; Mismatches 302; Indels 0; Gaps 0;

QY 172 GATPAGAAATGTCTCGAGCTGTTATGAGGGAATGACGCTGTCTTACGTCATATCATTT 231
Db 342 GACAGGACGTTCAAGATATTTAGTCAATGGCAATGGGCGGAGCTGTGTCATATCATATA 401
QY 232 TCACACTACTATAGGAGCAAAACGGGAAACGAAACGACACCATTTAGTTACATGGCTGAG 291
Db 402 GTGACGAGCATTTGATGGGAGAAATGGCGAGGCAAGCAGACCATTTAGTTACATGGCTGAG 461
QY 292 CGGGTTGTTGGAACAGCTTCATTCGGGATTTGTTTTCAGGCGAAATGCTTGGAAATCGGA 351
Db 462 CGGGTGTAGTGTATCGGTCCTTCGAAACCGTTTTCAGGCGCAAGTGTCTTGAATCTGGT 521
QY 352 GAATCAGTAGCCATTAAGAAAGGTTCTTCAAGATGCGAGCTATTAAGAAACCGTGTGTTGCAA 411
Db 522 GAGACGCTAGCTATAAAGAGGTTCTTCAAGACAGAGATACAGAAATCGTGAAGTGCAA 581
QY 412 CTATATGGACCAATGATCAGCCCAATATGCTATCTCTTGAAGACATGTTTCTTCTCTACA 471
Db 582 ACCATGCGAGTGTGTCACCAACCAAAATGTGGTGGCTCTAAGACATGTTTCTTCTCAAG 641

QY 472 ACGGTAGAGATGAGCTCTTCTCAACCTGTTTATGGAGTATGTACCTGAGACTTTTATAC 531
Db 642 ACTGAGAAGAGGAGCTTTACCTCAATTTGGTGTGCTTGGATATGACCGGAGACTGCTCAT 701
QY 532 CGGGTTTTGAGGCACTATACGTAGTCTTAATCAGAGATGCGCAATTTTCTATGTCAAGCTT 591
Db 702 CGTGTCTCATCAACATTTCAACCAAGATGAACCCAGCGCATGCGCTTTGATTTATGCAAACTG 761
QY 592 TACACATATCAATCTTTAGAGGTTTGGCTTACATCCATCTACTGTTCCCGGCTGTTGCCAC 651
Db 762 TATATGTATCAGATTTGTAGAGCTTTGGCATATTTTCAACAGCATTTGGAGTGTGCCAC 821
QY 652 AGAGATGTGAACACCAAAATCTCTTGGTTGATCCCTTGACCCATCAGGTTTAAGCTGTGT 711
Db 822 AGGACATTTAAGCCGCAAAATCTCTCGTTAATCTCTATACCAATCAGCTAAATTTGTGT 881
QY 712 GATTTTGAAGTGCAGAAAGTATTTGTCAAAGTGGAACCAAAATATATATATCTGCTCC 771
Db 882 GACTTTGGCAGCGCAAGGTTCTGTTAAAGGCGAAACCAACATTTCTTACATCTGTTCT 941
QY 772 CGTTATATCGTGTCTCCAGAACTCATCTTTGGGCGCACAGAGTATACAGCATCCATAGAT 831
Db 942 AGGTACTCAGAGCTCCAGAGCTCATATTTGGTGTCTACTGAATATACAAACAGCATTTAT 1001
QY 832 ATATGCTCTGCTGTTGTGTACTTGGCAGAGCTTCTTTTGGCCAGCGGTTATTTCCAGGA 891
Db 1002 GTTGGGCTCTGCTGGCTGTGTGCTCGCTGAGCTCTTCTAGGACAGCTCTGTTCCCTGGA 1061
QY 892 GAAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCCAACTCGTGAA 951
Db 1062 GAAAGCGGTGTGTATCAGCTTGTGTAATCATCAAGGTTCTGGGCGACACCCACAGTGAA 1121
QY 952 GAAATTCAGTGTATGAACCCGAACTTACAGATTTTAGGTTCCCAAAATCAAGCTCAC 1011
Db 1122 GAAATTAAGTGTGAATCCAAATATATCCGAGTTTAAATTCGCGAAATCAAGCTCAC 1181
QY 1012 CTTGGCACAAGGTTTTTTCATAAACGATGCTCCAGAGCAATAGACCTTGCATCTCG 1071
Db 1182 CATGGCATAAGATTTCCATAAAGGATGCTGCTGAAGCGGTAGATCTCGTGTCCAG 1241
QY 1072 CTTCTTCAATATTCACCAAGTCTAGCTGCACTGCGCTCGAAGCATGTGCTCATCGGTTT 1131
Db 1242 CTTCTGCACTACTCACCAAACTTCCGTCGACTGCTTTTGGAAAGCATTTGGTCCATCGGTT 1301
QY 1132 TTCAATGAACTCCGAGAGCCAAACCGCTCTTCCAAATGCTCGTCCATTTACCGCATTTG 1191
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QY 1192 TTCAATTTTCAAAAC 1204
Db 1362 TTCAATTTTAAAGC 1374

RESULT 5

US-09-854-731-9
; Sequence 9, Application US/09854731
; Patent No. 6794561
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 9
; LENGTH: 1814
; TYPE: DNA
; ORGANISM: Zea mays
US-09-854-731-9

Query Match 34.1%; Score 549.8; DB 4; Length 1814;
 Best Local Similarity 70.8%; Pred. No. 1.6e-154;
 Matches 731; Conservative 0; Mismatches 302; Indels 0; Gaps 0;

QY 172 GATAAGGAATCTCTGACGCTGTTATGAGGGAATGAGCGTGTACTGGTCATATCAT 231
 DB 342 GACAAGGAGCTTGAAGATATGTAGTCAATGCAATGGGCGGAGCGCTGGTCATATCAT 401
 QY 232 TCACACTATATAGGAGGCAAAACCGGAAACCAAGCAGACCATATTAGTTACATGCTGAG 291
 DB 402 GTGACGACCATTTGATGGGGAATGCGGAGGCAAGCAGACCATATTAGTTACATGCTGAG 461
 QY 292 CGGGTTGTTGGAACAGGTTTCATCGGATGTTTTCAGGCGAAATGCTTGGAACTGGA 351
 DB 462 CGGGTGGTAGGTCATCGGGCTTCGGAACCGTTTCCAGGCGCAAGTGTCTTGAACCTGGT 521
 QY 352 GAATCAGTAGGCAATTAAGAGGCTTTCGAAGATGAGCGCTATAAAACCGTGAGTTGCA 411
 DB 522 GAGACGCTAGCTATTAAGAGGCTTTCGAAGATGAGCGCTATAAAACCGTGAGTTGCA 581
 QY 412 CTAATGCGACCAATGATCACCACCAATGTCTCTCTTGAAGCACTGTTCTCTCTACA 471
 DB 582 ACCATGCGAGTCTTGACCAACCAATGTGGTCTCTAAAGCACTGTTCTCTCTACA 641
 QY 472 ACGAGTAGAGTAGCTCTCTCTCAACCTTGTATGAGATGATGATGAGCTGATGATGAT 531
 DB 642 ACTGAGAAAGAGGAGCTTCACTCAATTTGGTGTGATGATGATGATGATGATGATGAT 701
 QY 532 CGGGTTTGGGCACTATCTAGTCTTCAATCAGAGGATGCGCAATTTCTATGTCAGCTT 591
 DB 702 CGTGTCTCAACATTTACAAAGATGAAACGAGCGATGCTTTCATTTATGCAAACTG 761
 QY 592 TACACATATCAATCTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGGTTTGGCCAC 651
 DB 762 TATATGATCAGATTTGAGGCTTGGCATATCTCAACAGCATTTGGAGTGGCCAC 821
 QY 652 AGAGATGTGAACCAACCAATCTCTGTTGATGCTTGGACCCATCAGGTTAAGCTGTGT 711
 DB 822 AGGACATTAAGCGCAAAATCTCTGTTTATCTCTATACCCATCAGCTAAATTTGTGT 881
 QY 712 GATTTTGAAGTGCAAAAGTATTTGTCAGAGTGAACCAACATATCATATATCTGCTCC 771
 DB 882 GACTTTGGGCGCGGAAAGTCTCTGTTAAAGCGCAACCAACATTTCTTACATCTGTTCT 941
 QY 772 CGTTATTTATCGTCTCCAGAACTCATCTTTGGCGCACAGAGTATACAGCATATCATAGAT 831
 DB 942 AGGTACTACAGCTTCCAGAGCTCATATTTGGTGTCTATGATATACACAGCCATTTGAT 1001
 QY 832 ATATGCTCTGCTGGTGTGATCTGCGAGAGCTTCTTCTGGCCAGCCGTTATTTCCAGGA 891
 DB 1002 GTTGGGTCTGCTGGCTGTGCTGCTGAGCTGCTTCTAGGACAGCTCTGTTCCCTGGA 1061
 QY 892 GAAATTCAGTTGATCAGCTTGTGAGATCATATAAGGTTCTTGGTACTTCCAACTGCTGA 951
 DB 1062 GAAACGGTGTGATCAGCTTGTGAAATCATCAAGGTTCTGGGACACACCCACAGCTGAA 1121
 QY 952 GAAATTCAGTGTATGAAACCGAACTTACACAGATTTTGTAGTTCCCAACAAATCAAGCTCAC 1011
 DB 1122 GAAATTCAGTGTATGAAATTCAGGATTTATACCGAGTTTAAATTCGCGCAATCAAGCTCAC 1181
 QY 1012 CTTGGGCAAGAGTTTTCATAAACGAGTGTCTCCAGAGCAATAGACTGCTGCTCTCGG 1071
 DB 1182 CCATGGCATAAGATATCCATAAAGGATGCTGCTGAGCGGTAGATCTGTTCCAGG 1241
 QY 1072 CTTCTTCAATATTCACAGTCTACGCTGCACTGGCTGCAAGAGATGCTCATCCGTTT 1131
 DB 1242 CTTCTGCACTACTACCAAAATCTCGGTGCACTGCTTTGGAAGCATTTGGTCCATCCGTT 1301
 QY 1132 TTTCAATGAACTCCGAGAGCAACCGCTCTTCCAAATGTCGTCATTTACCGCAATG 1191
 DB 1302 TTTGATGAACCTTCGGGATCAAAACACCGCTTACCAGATGGTGTCTTCTTCGCGCTCTC 1361

QY 1192 TTCAATTTCAAAC 1204
 DB 1362 TTCAATTTTAAGC 1374

RESULT 6
 US-09-347-801-13
 ; Sequence 13, Application US/09347801
 ; Patent No. 6262345
 ; GENERAL INFORMATION:
 ; APPLICANT: Allen, Steve
 ; APPLICANT: Lee, Jian Ming
 ; TITLE OF INVENTION: Plant Protein Kinases
 ; FILE REFERENCE: BB-1171
 ; CURRENT APPLICATION NUMBER: US/09/347,801
 ; EARLIER FILING DATE: 1999-07-02
 ; EARLIER APPLICATION NUMBER: 60/092,438
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 13
 ; LENGTH: 1429
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1202)
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1237)
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1297)
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1340)
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1376)
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1410)
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1416)
 ; US-09-347-801-13

Query Match 32.4%; Score 523.4; DB 3; Length 1429;
 Best Local Similarity 69.6%; Pred. No. 1.2e-146;
 Matches 723; Conservative 0; Mismatches 313; Indels 3; Gaps 1;

QY 171 TGATAAGGAATGTCTGACGCTGTTATGAGGGAATGACGCTGTACTGGTCATATCAT 230
 DB 224 TGATAGAGAAATGGAGCCAGTTGTTGATGGCAACGGAACGAGACAGGACATATCAT 283
 QY 231 TTCCACTACTATAGGAGGCAAAAAACGGCAACCAAGCAGACCATATTAGTTACATGCTGGA 290
 DB 284 TGTGACTACCATTTGGGGTAGAAATGGTCAGCCCAAGCAGACTATAAGCTACATGGCAGA 343
 QY 291 CGGGTTGTTGGAACAGGTTTCATTCGGGATGTTTTCAGGCGAAATGCTTGGAAACTGG 350
 DB 344 CGGTGTTGTTAGGGCATGGATCAITTTGGAGTTGTCTTCAGGCTAAGTGTCTTGGAAACCGG 403
 QY 351 AGAATCAGTACGCCATTAAGAAAGGCTTTCAGAGATCGACGCTATAAAAAACCGTGAGTTGCA 410
 DB 404 TGAACCTGTGCTATCAAAAAGGTTCTTCAAGACAGAGGTACAGAACCGGAGACTGCA 463
 QY 411 ACTAATGCGACCAATGGATCACCACCAATGTCTCTCTTGAAGCACTGTTCTCTCTAC 470
 DB 464 AACATGCGCTCTTGTGACCAACCAATGTCTGTTGCTTTGAAGCACTGTTCTCTTCAAC 523
 QY 471 AACGAGTAGATGAGCTCTCTCAACCTTGTATGAGGATGTACCTGAGACTTTATA 530

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Db 524 CACTGAAAGGATGAACATATACCTTAATTTGGTTCTCGAATATGTTCTCGAAACAGTTAA 583
QY 531 CCGGGTTTTGAGGCACTATAGTTCTTAATCAGAGATGCCAATTTTCTATGTCAAGCT 590
Db 584 TCGGGTGATAAACATATACAAAGTTTACCAAGGATGCCACTGATATATGTGAAC 643
QY 591 TTACACATATCAATCTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGGTGTTTGCCA 650
Db 644 CTATACATACCAGATCTTTAGGGCGTTATCTTATATTCATCGTTGTTGGAGTCTGCCA 703
QY 651 CAGAGATGTGAACCAAAATCTCTGTTGATCCCTTGACCCATCAGGTTAAGCTGTG 710
Db 704 TCGGGATATCAGCCCTCAAAATCTATTTGGTCAATCCACACTCAGGCTTAAATATG 763
QY 711 TGATTTTGAAGTGCAAAAGTATTTGTTCAAAAGTGAAACCAATATATATATCTGCTC 770
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QY 771 CCGTTATTTATCGTGTCTCCAGAACTCATCTTTGGCGCCACAGATATACAGCATCCATAGA 830
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QY 831 TATATGCTGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 890
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QY 1011 CCCTTGGCAAGGTTTTTCATAAACGATGCTCCAGAGCAATAGACCTTGCATCTCG 1070
Db 1064 TCCATGGCAAGATCTTCCATAGGCGATGCGCTCCAGAGGCTGTTGATTTGGTATCAAG 1123
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QY 1131 ---TTTCAATGAACTCCGAGGCAAAACGCGCTCTTCCAAATGGTGTGCTCAATACCGCC 1187
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QY 1188 ATTGTTCAATTCACAA 1206
Db 1244 AACTATTAATTCAAACCA 1262

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RESULT 7
US-09-854-731-13
; Sequence 13, Application US/09854731
; Patent No. 6794561
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1429
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1202)

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; NAME/KEY: unsure
; LOCATION: (1237)
; NAME/KEY: unsure
; LOCATION: (1297)
; NAME/KEY: unsure
; LOCATION: (1340)
; NAME/KEY: unsure
; LOCATION: (1376)
; NAME/KEY: unsure
; LOCATION: (1410)
; NAME/KEY: unsure
; LOCATION: (1416)
; US-09-854-731-13

Query Match      32.4%; Score 523.4; DB 4; Length 1429;
Best Local Similarity 69.6%; Pred. No. 1.2e-146;
Matches 723; Conservative 0; Mismatches 313; Indels 3; Gaps 1;

QY 171 TGATAAGGAAATGTCTGCAGCTGTTTATTGAGGGAATGACGCTGTCTGTTTACCTGGTCAATCAT 230
Db 224 TGATAGAGAAATGGAAGCCACAGTTTGTTCATGGCAACGGAACGGAGACAGGACATATCAT 283
QY 231 TTCCACTACTATAGAGAGCAAAAACGGCGAAACCAAGAGCAGACATTAGTTACATGCTGA 290
Db 284 TGTGACTACCATTTGGGGGTAGAAATGGTCAGGCCAAGCAGACTATAAGCTACATGTCGAGA 343
QY 291 GCGGGTTGTTGNAACAGGTTTCATTCGGGATTCGTTTTCAGGCGAAATGCTTGGAAACTGG 350
Db 344 GCGTGTGTAGGGCATGGATCATTTGGAGTTGTCTTCCAGGCTAAGTGTCTTGGAAACCGG 403
QY 351 AGAATCAGTATGAGCATTTAAAGAGTCTTGCAGAGATCGACGCTATATAAAACCGTGAGTTGCA 410
Db 404 TGAACCTGTGCTATCAAAAGGTTCTTCAAGACAAAGAGGTACAAGAACCGGAGCTGCA 463
QY 411 ACTAATGCAACCAATGAGTACCCAAATGTCATCTCTTGAAGCACTGTTTCTTCTCTAC 470
Db 464 AACAAATGCGCTTCTTGGACCCCAAAATGTCGTTGCTTTGNAAGCACTGTTTCTTTTCAAC 523
QY 471 AACGAGTATGAGATGAGCTCTCTCTCAACCTTGTATGAGAGTATGTACCTGAGACTTTATA 530
Db 524 CACTGAAAGGATGAACATATACCTTAATTTGGTTCTCGAATATGTTCTTGAACAGTTAA 583
QY 531 CCGGGTTTTGAGGCACTATATAGTTCTTAATCAGAGGATGCCAATTTTCTATGTCAAGCT 590
Db 584 TCGGGTGATAAACCAATTTACCAAGTTTAAACCAAGGATGCCACTGATATATGTGAAACT 643
QY 591 TTACACATATCAAACTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGGTGTTTGCCA 650
Db 644 CTATACATACCAGATCTTTAGGGCGTTATCTTATATTCATCGTTGTTTGGAGTCTGCCA 703
QY 651 CAGAGATGTGAACCAACCAAAATCTCTTGGTTGATCCCTTGGACCATCAGGTTAAGCTGTG 710
Db 704 TCGGGATATCAAGCTTCAAAATCTATTTGGTCAATCCACACTCAGGTTAAATATG 763
QY 711 TGATTTTGAAGTGCAAAAGTATTTGTTCAAAAGTGAAACCAACATATATATATCTGCTC 770
Db 764 TGACTTTGGAAGTGCAAGGTTTGGTAAAGGCGAACCATAATATATATATATATATGTTTC 823
QY 771 CCGTTATTTATCGTGTCTCCAGAACTCATCTTTGGCGCCACAGATATACAGCATCCATAGA 830
Db 824 TAGATATATAGAGCACCTGAGCTCATATTTGGCGCAACTGAAATATATATATATATG 883
QY 831 TATATGCTGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 890
Db 884 CGTCTGTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 943
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Db 944 TGAGAGTGGAGTTGATCAACTTGTGAGATCATCAAGGTTCTGGGCACTCCAAAGGGA 1003
QY 951 AGAAATTCAGTTGATCAGCTTGTGGAGATCAACAGATTTTGGTACTCCCAAACTCAAGCTCA 1010
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QY 1011 CCCTTGGCACAAGGTTTTCATAAAGGATGCTCCAGAGCAATAGACCTTGCATCTCG 1070
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QY 1071 GCTTCTTCAATATTCACCAAGTCTACGCTGCACTGGCTCGAAGCATGTGCTCATCCGTT 1130
DB 1124 ACTACTACATATCTCCCTTACTGCTGGTGCAAGTTTGTAGTGTCTTGGAGCGACCTTT 1183
QY 1131 ---TTTCAATGAATCCGAGAGCCAAACGCCGCTTCCAAATGGTGTGCTTACCGCC 1187
DB 1184 TCCCTTGGAGCAATTCGNGATCCAAATCCTCGCTTGCCAAATGGCGCATCCNTCCAA 1243
QY 1188 ATTGTTCAATTTCAACAA 1206
DB 1244 AACTATTAATTCAAACCCA 1262

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US-09-489-765A-3
; Sequence 3, Application US/09489765A
; Patent No. 6323029
; GENERAL INFORMATION:
; APPLICANT: Madeline M. Butler
; APPLICANT: Robert McKay
; APPLICANT: Brett P. Monia
; APPLICANT: Jacqueline Wyatt
; FILE OF INVENTION: ANTISENSE MODULATION OF GLYCOGEN SYNTHASE KINASE 3 BETA EXPRES
; CURRENT APPLICATION NUMBER: US-09/489,765A
; CURRENT FILING DATE: 2000-01-19
; NUMBER OF SEQ ID NOS: 85
; SEQ ID NO 3
; LENGTH: 1389
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (40)... (1302)
US-09-489-765A-3

Query Match 23.9%; Score 385.2; DB 3; Length 1389;

Best Local Similarity 65.5%; Pred. No. 4.4e-105;
Matches 596; Conservative 0; Mismatches 308; Indels 6; Gaps 2;

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DB 220 GTGATGGAAATGGATCAITTTGGTGTGTATATCAAGCCAACTTTGTGATTCAGAGAA 279
QY 355 TCAGTAGCCATTAATAAGGCTTTGCAAGATCGACGCTATAAAACCGGTGAGTTGCAACTA 414
DB 280 CTGGTCGCCATCAAGAAAGTATTGCGAGCAAGAGATTTAAGAAATCGAGAGCTCCAGATC 339
QY 415 ATGCGACCAATGGATCCCAATGTCATCTCTTGAAGCACTGTTTCTCTC---TACA 471
DB 340 ATGAGAAAGTAGATCACTGTAAACATAGTCCGATTCGCTTATTTCTTCTACTCCAGTGT 399
QY 472 ACGAGTAGAGTAGACTCTTCTCAACCTGTTGATGGAGTAGTGTACCTCGAGACTTTATAC 531
DB 400 GAGAGAAAGATGAGGTCTATCTTATCTGGTGTGAGTATGTTCCGGAACAGATATAC 459
QY 532 CGGGTTTGGAGCATACTAGTTTCTAATCAGAGGATGCCAAATTTCTATGTCAAGCTT 591
DB 460 AGAGTTGCCAGACACTATAGTCGAGCAAAACAGAGGCTCCCTGTGATTTATGTCAAGTTG 519
QY 592 TACATATCAATCTTTAGAGTTTGGCTTACATCCATGTTCCCGGTGTTGGCCAC 651
DB 520 TATATGTATCAGCTGTTCCGAGTTTAGCTATATCCATTCCTTT---GGAATCTGCCAT 576
QY 652 AGAGATGTGAACACCAAAATCTCTGGTGTGATCCCTTGACCCATCAGGTTAAGCTGTGT 711
DB 577 CGGATATTAACCCGAGAACCTCTGTGTGATCCTGATCTGCTGTATTAACCTCTGT 636

QY 712 GATTTGGAAGTGCARAAGTATTGGTCAAGGTGAACCAACATATCATATATCTGCTCC 771
DB 637 GACTTTGGAAGTGCARAAGCAGCTGGTCCGAGGAGAACCAATGTTTCGTATATCTGTCT 696
QY 772 CGTTATTATCGTGTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGCATCCCATAGAT 831
DB 697 CGGTACTATAGGCAACAGAGTTGATCTTTGGAGCCACTGATTATACCTCTAGTATAGAT 756
QY 832 ATATGGTCTGCTGGTGTGTACTGGCAGAGCTTCTTCTTGGGCCAGCCGTTATTTCCAGGA 891
DB 757 GTATGGTCTGCTGGTGTGTGTGGCTGAGCTGTTACTAGGACCAACCAATATTTCCAGGG 816
QY 892 GAAATTCAGTTGATCATCTTGTGGAGATCATAAAGTTCTTGGTACTCCCACTCGTGA 951
DB 817 GATAGTGGTGGATCAGTTGTGTAAGAAATATCAAGGTCTCTGGGAATCCCAACAGGGAG 876
QY 952 GAAATTCGATGTATGAACCCGAACTTACACAGATTTTGGTTCCCAACAAATCAAGCTCAC 1011
DB 877 CAATCAGAGAAATGAACCCAACTACACAGAAATTAATTTCCCTCAATTAAGGCACAT 936
QY 1012 CTTTGGCACAAGGTTTTTCATAAAGGATGCTCCAGAGCAATAGACCTTGCATCTCGG 1071
DB 937 CTTTGGACTAAGGTCTTCCGACCCGAACTCCACCGAGGCAATTCACCTGTGTAGCCGT 996
QY 1072 CTTCTTCAATATTCACCAAGTCTAGCTGCACTGGCTCGAGCATGTGCTCATCCGTT 1131
DB 997 CTGCTGGAGTATACACCAACTGCCGCACTAACACCACTGGAAGCTTTGTGCACATTCAT 1056
QY 1132 TTCAATGAATCCGAGAGCCAAACGCCGCTCTTCCAAATGCTGTCATTCACCGCATTG 1191
DB 1057 TTTGATGAATTCGGGACCCCAATGTCAACATCCNAATGGCGAGACACACCTGCATC 1116
QY 1192 TTCAATTTCA 1201
DB 1117 TTCAACTTCA 1126

RESULT 9

US-09-016-434-1414
; Sequence 1414, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
; APPLICANT: Janice Au-Young
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
; TITLE OF INVENTION: PATHWAY GENE EXPRESSION
; NUMBER OF SEQUENCES: 1490
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,434
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0002 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555

QY 956 TTGATGATGAAACCGAACTACAGATTTTAAAGTTTCCACAAATCAAAGCTCACCCCTT 1015
 DB 1457 TCAGAGAAATGAACCCAACTACAGAAATTTAAATCCCTCAATTAAGGCACATCCCTT 1516
 QY 1016 GGCACAAGGTTTTTCAATAAAGCGATCCCTCCAGAACAAATAGACCTTGCATCTCGGCTTC 1075
 DB 1517 GGACTAAGGCTTCCGACCCGAACTCCACCGGAGCAATTCACCTGTGTAGCCGCTGC 1576
 QY 1076 TTCAATATTCAACCAAGCTACGCTGCACTGCGCTCGAAGCATGTGCTCATCCGTTTTTCA 1135
 DB 1577 TGAGATATACACCAACTGCGCGACTAACCACTGGAAGCTTGTGCACATTCATTTTTTG 1636
 QY 1136 ATGAATTCGAGACCAAAAGCGCGCTTCCAAATGGTCTCCATTACCGCCATTGTTC 1195
 DB 1637 ATGAATTCGAGACCAAAATGTCAAACTACCAAAATGGGAGACACACCTGCACCTTCA 1696
 QY 1196 ATTCA 1201
 DB 1697 ACTTCA 1702

RESULT 12
 US-09-216-958-1
 ; Sequence 1, Application US/09216958
 ; Patent No. 6248559
 ; GENERAL INFORMATION:
 ; APPLICANT: Akihiko TAKASHIMA et al.
 ; TITLE OF INVENTION: SCREENING METHOD FOR THERAPEUTIC AGENTS AGAINST
 ; TITLE OF INVENTION: ALZHEIMER'S DISEASE (AS AMENDED)
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WENDEROTH, LIND & PONACK
 ; STREET: 805 Fifteenth Street, N.W., #700
 ; CITY: Washington
 ; COUNTRY: D.C.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch,
 ; MEDIUM TYPE: 1.44 mb
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/216,958
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/461,018
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warren M. Cheek, Jr.
 ; REGISTRATION NUMBER: 33,367
 ; REFERENCE/DOCKET NUMBER:
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE:
 ; TELEFAX:
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 2088 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to genomic RNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: human being
 ; US-09-216-958-1

Query Match 23.8%; Score 384.4; DB 3; Length 2088;
 Best Local Similarity 65.6%; Pred. No. 9.8e-105;
 Matches 594; Conservative 0; Mismatches 306; Indels 6; Gaps 2;

QY 299 TTGGAACAGGTTCAITTCGGGATTTGTTTTTCAGCGAAATGCTTGGAACTGGAGATCAG 358
 DB 800 TTGGAATTCGATCAITTCGGTGTGTATATCAAGCCAACTTTGTGATTCAGGAACTGG 859
 QY 359 TAGCCATTAAAAAGGCTTTGCAAGATCGACGCTATAAAAAACCGTGAGTTGCAACTAATGC 418
 DB 860 TCGCCATCAAGAAAGATTTGCAAGACAGAGATTTAAGAAATCGAGAGCTCCAGATCATGA 919
 QY 419 GACCAATGGATCACCACCAATGTCATCTCTCAAGCACCTGTTCTTCTC- -TACAACA 475
 DB 920 GAAAGTAGTACCTGTACATAGTCCGATTCGGTTATTTCTTCTACCTCAAGTGGTGA 979
 QY 476 GTAGAGATGAGCTCTTCCTCAACCTTTGTTATCGAGTATGCTACCTGAGACTTTATACCGG 535
 DB 980 AGAAGATGAGCTCTATCTTAATCTGGTCTGCACTATGTTCCGGAACAGATATACAGAG 1039
 QY 536 TTTTGAGGCACTATATCTAGTCTTAATCGAGAGATGCAATTTTCTATGTCAGACTTTTACA 595
 DB 1040 TTGCCAGACACTATAGTCGAGCCAAACAGACGCTCCCTGTGATTTATGTCAAGTTGTATA 1099
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 DB 1100 TGTATCAGCTGTTCGAGTTTAGCTTATCCATTCCTTT- -GGAATCTGCCATCGG 1156
 QY 656 ATGTGAACCAACAAATCTCTTGGTTGATCCCTTGACCCATCAGGTTAAGCTGTGTGATT 715
 DB 1157 ATATTAAACCGCAGAACCTCTTGTGGATCTCTGATCTGCTGTTATTAACCTGTGACT 1216
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 QY 776 ATTATCGTCTCCAGAACTCATCTTTGGCGCACAGAGTATACAGATCCATAGATATAT 835
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 QY 836 GGTCTGCTGTTGTGTACTTGGCAGAGCTTCTTTCTGGCCAGCGCTTATTTCCAGGAGAAA 895
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 QY 896 ATTCAGTTGATCAGCTTTGGAGATCATAAAGTTCTTGGTACTCCTCAACTCGTGAAGAAA 955
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 DB 1637 ATGAATTACGGGACCAAAATGTCAAACTACCAAAATGGGCGAGACACACCTGCACCTTCA 1696
 QY 1196 ATTCA 1201
 DB 1697 ACTTCA 1702

RESULT 13
 US-09-566-921-24
 ; Sequence 24, Application US/09566921
 ; Patent No. 6682888
 ; GENERAL INFORMATION:
 ; APPLICANT: Loring, Jeanne F.
 ; APPLICANT: Tingley, Debora W.
 ; APPLICANT: Edwards, Carla M.

Qy	663	ACCAAAATCTCTTGGTTGATCCCTTGACCCATCAGGTTAAGCTGTGCTGATTTGGAAG	722
Db	829	GCCCAGAACTGCTGTGTGGACCTGCACCTGCTCTCAAGCTCTGCGATTTTGGCAG	888
Qy	723	TGCAAAAGTATTGGTCAAAGGTGAACAAACATATCATATATCTGCTCCCGTTATTATCG	782
Db	889	TGCAAGCAGTTGTTCCGAGGGAGCCCATGTCTCTACATCTGTCTCGCTACTACCG	948
Qy	783	TGCTCCAGAACTCATCTTTTGGCGCCACAGAGTATACAGCATCCANAGATATATGCTCTGC	842
Db	949	GGCCCCAGAGCTCATCTTTGAGGCCACTGATTACACCTCATCCATCGATGTTTGGTCAGC	1008
Qy	843	TGGTTGTGTACTGGCAGAGCTTCTTCTTGGCCAGCCGTTATTTCCAGGAGAAAATTCAGT	902
Db	1009	TGGCTGTGTACTGGCAGAGCTCTCTTTGGGCCAGCCCATCTTCCCTGGGACAGTGGGGT	1068
Qy	903	TGATCAGCTGTGGAGATCATATAAGGTTCTTGGTACTTCCAACCTCGTGAAGAAATTCGATG	962
Db	1069	GGACAGCTGTGGAGATCATCAAGGTGCTGGGAACACCAACCCGGGAAACAAATCCGAGA	1128
Qy	963	TATGAACCCGAACATACACAGATTTTAGTGTCCCAACAATCAAAGCTCACCTTGGCACA	1022
Db	1129	GATGAACCCCAACATACAGGAGTTCCATAGTTCCCTCAGATTAAGCTCACCCCTGGACAA	1188
Qy	1023	GGTTTTTCATAAACGGATGCTCCAGAAAGCAATAGACTTGGCACTCGGGTCTTCTCAATA	1082
Db	1189	GGTGTTCAAATCTCGAACCGCGCCAGAGGCCATCGCGCTCTGCTCTAGCCTGCTGGAGTA	1248
Qy	1083	TTCAACCAAGTCTACGCTGCACTGGCTCGAGCATGTGCTCATCCGTTTTTCAATGAAC	1142
Db	1249	CACCCCATCTCAAGGCTCTCCCACTAGAGCCTGTGGCAGAGCTCTTTTGAATGAAC	1308
Qy	1143	CCGAGGCCAAACGCCCGTCTTCCAAATGGTGTGCCAATTACCGCCATTGTTCAAATTTCAA	1202
Db	1309	CGCATGTCTGGGAACCCAGCTGCTTAACACCGGCCACTTCCCCCTCTCTTCAACTTCAG	1368
Qy	1203	ACAGAGTTAGGTGGAGCTTCAATGGAGCTTAATCAACAGGCTAATACCTGAGCATGTGAG	1262
Db	1369	TGCTGGTGAATCTTCCATCCMACCGTCTCTCAAGCCATTTCTATCCCTCTCTCACTTGAG	1428
Qy	1263	ACGACAAATGAGCAC	1277
Db	1429	GTCCCCAGCGGGCAC	1443

RESULT 15
US-08-602-264A-2
; Sequence 2, Application US/08602264A
; Patent No. 5837853
; GENERAL INFORMATION:
; APPLICANT: Akhiko TAKASHIMA et al.
; TITLE OF INVENTION: PREVENTIVE OR THERAPEUTIC AGENTS FOR
; TITLE OF INVENTION: ARZHEIMER'S DISEASE, A SCREENING METHOD OF
; TITLE OF INVENTION: tau-PROTEIN KINASE I ORIGINATED FROM HUMAN BEING (AS AMENDED)
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; COUNTRY: D.C.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch,
; MEDIUM TYPE: 144 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/602,264A
; FILING DATE: February 20, 1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:

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Total number of hits satisfying chosen parameters: 12134778

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	713.2	44.2	1831	19	US-10-437-963-98579
4	710.4	44.0	1143	9	US-09-938-842A-875
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6	710.4	44.0	1490	21	US-10-477-687-12
7	706.2	43.8	1726	18	US-10-425-114-12807

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9	701.6	43.5	1673	9	US-09-854-731-15
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18	676.8	41.9	1614	18	US-10-425-114-17458
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20	676.8	41.9	1868	20	US-10-425-115-32308
21	673	41.7	1698	18	US-10-425-114-35222
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23	665	41.2	1828	20	US-10-425-115-32310
24	659.2	40.8	1808	20	US-10-739-930-4849
25	657.4	40.7	1936	19	US-10-437-963-24168
26	645	40.0	2103	20	US-10-425-115-22953
27	621.8	38.5	1711	18	US-10-425-114-22299
28	620.2	38.4	1600	18	US-10-425-114-34808
29	620.2	38.4	1645	18	US-10-425-114-4124
30	618.6	38.3	1818	20	US-10-425-115-148434
31	585.6	36.3	1766	18	US-10-425-114-26106
32	585.6	36.3	1807	19	US-10-767-701-14202
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35	581.2	36.0	1672	18	US-10-425-114-32862
36	579.6	35.9	2573	20	US-10-425-115-111277
37	573.8	35.6	2794	19	US-10-437-963-9996
38	571.2	35.4	1589	18	US-10-424-599-67975
39	571.2	35.4	1589	18	US-10-425-114-29569
40	571	35.4	1833	20	US-10-739-930-5123
41	567.6	35.2	1849	16	US-10-292-408-2
42	563	34.9	2165	19	US-10-437-963-24107
43	562.2	34.8	1635	18	US-10-425-114-9488
44	562.2	34.8	1867	18	US-10-424-599-81473
45	560.4	34.7	1817	18	US-10-425-114-8223

ALIGNMENTS

RESULT 1
US-10-764-138-6
; Sequence 6, Application US/10764138
; Publication No. US20050081266A1
; GENERAL INFORMATION:
; APPLICANT: Sudwestdeutsche Saatzeucht-SWS
; APPLICANT: Advanta Seeds B.V.
; TITLE OF INVENTION: Modulation of Storage Organs
; FILE REFERENCE: 026-1
; CURRENT APPLICATION NUMBER: US/10/764,138
; CURRENT FILING DATE: 2004-01-23
; PRIOR APPLICATION NUMBER: US/09/578,194
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; TYPE: DNA
; LENGTH: 1636
; ORGANISM: Arabidopsis sp.
; FEATURE:
; NAME/KEY: mRNA
; LOCATION: (1)...(1636)
; OTHER INFORMATION: strain Columbia ecotype
; OTHER INFORMATION: taxon:3702
; OTHER INFORMATION: tissue type leaves
; OTHER INFORMATION: clone lib lambda ZAPII development stage young shoots
; PUBLICATION INFORMATION:
; AUTHORS: Dornelas, M.C., Schwebel-Dugue, N., Thomas, M., Lecharny, A. and Kreis, M.
; TITLE: Three New cDNAs Related to SG/GSK-3 (Shaggy/Glycogen synthase kinase-3)
; TITLE: from Arabidopsis thaliana (Accession No. X94938, x94939 and X99696) (PGR97-

Instant
Case

; TITLE: 008)		; JOURNAL: Plant Physiol.	
; VOLUME: 113		; ISSUE: 1	
; PAGES: 306-306		; DATE: 1997-01-01	
; DATABASE ACCESSION NUMBER: genbank/X94938		; DATABASE ENTRY DATE: 1998-02-13	
; RELEVANT RESIDUES: (1)...(1636)		US-10-764-138-6	
Query Match		60.2%; Score 972.2; DB 21; Length 1636;	
Best Local Similarity		77.0%; Pred. No. 6.3e-260;	
Matches 1234; Conservative		0; Mismatches 343; Indels 26; Gaps 3;	
QY	38	TTCAAGTGGTGGAGAGAAAGAG-TAAAAAGCACATGCGCTCATATTACATTGGGGCCT	96
DB	9	TTCAAGTGGAGAGAGAAAGTTAGAGCTGTAAAGACATGACTTTGATACCATTTGGGGCCT	68
QY	97	CAGCCTCATGC-----TCTTGCTCCGCGCTGCAGCTTCACGACGCGACGCTTTGAAA	150
DB	69	CCTCAGCCTCGTCTTTAGCTCTCAGCCCGCATCTTCACGCGCGAGATTCTTTGAAA	128
QY	151	CGCGCTCTGAATTGGATTCTGATAAGGAAATGCTGCAGCTGTTATTGAGGGAATGAC	210
DB	129	CGTGTCCCGATATAGACAACGACAGAGAAATGCTGCTGCTTTATAGAGGAATGAT	188
QY	211	GCTGTTACTGCTCATATCAATTTCCACTATATAGGAGGCAAAACCGCGCAACCAAGCAG	270
DB	189	GCTGTTTACCGGTACATATTTCTACTACAAATTTGGAGGCAAAATGTTGAACCTAAACAG	248
QY	271	ACCAATTAGTTACATGCTGAGCGGTTTGGAAACAGGTTTCAATTCGGGATTGTTTTTCAG	330
DB	249	ACCAATTAGTTACATGCGCGAACGTGTTTGGAAACAGGATCAATTCGAATTTGATTTCCAG	308
QY	331	CGAAATGCTTGGAACTGAGGAATCAGTAGCCATTAAGAAAGTCTTTGCAAGATCGACGC	390
DB	309	GCAAAATGCTTGGAACTGAGGAATCAGTAGCCATTAAGAAAGTCTTTGCAAGATCGCGT	368
QY	391	TATAAAACCGTGAGTTGCAACTAATGCGACCAATGATGATGATGATGATGATGATGATG	450
DB	369	TATAAAACCGTGAGTTGCAACTAATGCGACCAATGATGATGATGATGATGATGATGATG	428
QY	451	AAGCAGTGTCTCTCTCAACAGGATGAGATGAGCTTCTCAACCTTTGATTTGAGGAG	510
DB	429	AAGCAGTGTCTCTCTCAACAGGATGAGATGAGCTTCTCAACCTTTGATTTGAGGAG	488
QY	511	TATGTACCTGAGACTTTATACCGGGTTTGGAGGACTATATAGTTCTTAATCAGAGGATG	570
DB	489	TATGTACCTGAGACTTTATACCGGGTTTGGAGGACTATATAGTTCTTAATCAGAGGATG	548
QY	571	CCAAATTTCTATGCAAGCTTTACACATATCAAAATCTTTAGAGGTTTGGCTTACATCCAT	630
DB	549	CCTATCTTCTATGTCAAACTTTTACATACCAAAATCTTCAGAGGCTTGGCTTATATCCAT	608
QY	631	ACTGTTCCCGGTTGTTGCCACAGAGATGCAAAACCAAAATCTTTGTTGTTGATCCCTTG	690
DB	609	ACTGTTCCCGGTTGTTGCCACAGAGATGCAAAACCAAAATCTTTGTTGTTGATCCCTTG	668
QY	691	ACCCATCAGGTTAAGCTGTGATTTTGGAAAGTGCAAAAGTATTGGTCAAAGGTGAACCA	750
DB	669	ACCCATCAGGTTAAGCTGTGATTTTGGAAAGTGCAAAAGTATTGGTCAAAGGTGAACCA	728
QY	751	AACATATCATATCTGCTCCGTTTATATCGTGCTCCAGACTCATCTTTGGCGGCACA	810
DB	729	AACATATCATATCTGCTCCGTTTATATCGTGCTCCAGACTCATCTTTGGTGCCACA	788
QY	811	GAGTATACAGATCCATAGATATATGTTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTT	870
DB	789	GAGTATACATCCATAGATATATGTTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTT	848
QY	871	GGCCAGCGGTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTT	930

RESULT 2

US-10-292-408-25
; Sequence 25, Application US/10292408
; Publication No. US20030182692A1
; GENERAL INFORMATION:
; APPLICANT: VAN THIELEN, NICHA
; APPLICANT: DA COSTA E SILVA, OSWALDO
; APPLICANT: CHEN, RUOYING
; TITLE OF INVENTION: OF USE IN PLANTS
; TITLE OF INVENTION: OF USE IN PLANTS
; FILE REFERENCE: 16313-0178
; CURRENT APPLICATION NUMBER: US/10/292,408
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: 60/346,096
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 1744
; TYPE: DNA
; ORGANISM: Glycine max
US-10-292-408-25

Qy	1135	AATGAAC	TCGAGAGCCAAAGCCCGTCTTC	CAAAATGGTGTGTCATATACCGCATGTGTC	1191
Db	1132	GATGAGCTT	CGCAACCAAAATGCCCGCTAC	TAAATGGCCGTCACATGCCCCCATCTTTTC	1191
Qy	1195	AATTTCAAA	CAAGAGTTAGTGGAGCTTCAAT	CGAGCTAATCAACAGGCTAATACCTGAG	1254
Db	1192	AAC	TTCAACAGAGTTAGCTGGAGCA	TACCTGAACTGATCAATAGGCTCATCCAGAG	1251
Qy	1255	CATGTGAG	CGACAAATGAG	1274	
Db	1252	CATATTAGG	CGCAGATGGG	1271	
RESULT 3					
US-10-437-963-98579/c					
; Sequence 98579, Application US/10437963					
; Publication No. US20040123343A1					
; GENERAL INFORMATION:					
; APPLICANT: La Rosa, Thomas J.					
; APPLICANT: Kovalick, David K.					
; APPLICANT: Zhou, Yihua					
; APPLICANT: Cao, Yongwei					
; APPLICANT: Wu, Wei					
; APPLICANT: Boukharov, Andrey A.					
; APPLICANT: Barbazuk, Brad					
; APPLICANT: Li, Ping					
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated					
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement					
; FILE REFERENCE: 39-21(53221)B					
; CURRENT APPLICATION NUMBER: US/10/437,963					
; CURRENT FILING DATE: 2003-05-14					
; NUMBER OF SEQ ID NOS: 204966					
; SEQ ID NO 98579					
; LENGTH: 1831					
; TYPE: DNA					
; ORGANISM: Oryza sativa					
; FEATURE:					
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96473C.1					
US-10-437-963-98579					
Query Match 44.2%; Score 713.2; DB 19; Length 1831;					
Best Local Similarity 79.5%; Pred. No. 1.2e-187;					
Matches 844; Conservative 0; Mismatches 218; Indels 0; Gaps 0;					
Qy	208	GAGCGTGT	TACTCGTCATATCATTTCCAC	TACTATAGGAGGCCAAAAACGGCAACCAAAG	267
Db	1591	GAGCGCTG	ACGGGTACATCATCTCCAC	CAACATCGCGGCAAGAACGGCGAGCCGAG	1532
Qy	268	CAGACCA	TATAGTTACATGGCTGACGGG	TGTGTGGAACAGGTTCAATTCGGGATTTGTTTT	327
Db	1531	CGGACA	TAATAGTTATATGTCGGGAGCGAG	TTGTAGGAATGTTCTTTTCGGGATTTGTTTC	1472
Qy	328	CAGCGMA	ATGCTTGGAACTGAGAACTGAGAA	TCAATGATAGCAATTAAGAGTCTTGCAGATCGA	387
Db	1471	CAGGCTA	AGTGCTTGGAGACGGGGGAAACGG	TGGCCATCAAGAAGGTGTTTGCAGGACCGG	1412
Qy	388	CGCTAT	ATAAAACCGTGAGTTGCAACT	AATGCGACCAATGATCACCACCAATGTCATCTCC	447
Db	1411	CGTTAC	AGAACCGTGAACCTGACGCT	TATGCGCGCAATGGAACCCCAATGTCATCTGC	1352
Qy	448	TTGAAG	CACCTGTTTTCTTCTCTACA	ACGAGTAGAGATGAGCTCTTCTCTCAACCTTGTATG	507
Db	1351	CTGAAG	CACCTGCTTCTTCTCAAC	CAACGAGGATGAGCTGTGTTCTGAACTTGTATG	1292
Qy	508	GAGTATG	TACTGAGACTTTATACCGGG	TTTTGAGGCACTATACTAGTTCTATACAGG	567
Db	1291	GAGTACG	TCCCTCGACACACTCTAC	CCGTGTCTCAAGCACTACAGCAATGCTAACCGAGCGG	1232
Qy	568	ATGCCA	ATTTCATGTCAAGCTTTAC	ACATATCAAAATCTTTAGAGGTTTGGCTTACATC	627
Db	1231	ATGCCA	TTGATGTGGAAGCTTTA	CACTATCACTATCAGCTTTTTCAGAGGTTAGCTTATTT	1172
Qy	628	CATACTG	TTTCCCGGTGTGTTGGCA	CAGAGATGTGAAACCAACCAAAATCTCTTTGGTTGATCCC	687

1171 CATACTGTTCCAGGAGTCTGCCACAGGATGTGAACCAACAAAATGTTTGGTTGATCCT 1112
 688 TTGACCCATCAGGTTAAGCTGTGTGATTTTGGAGTGCAAAAGTATGTGTCAAGGTGAA 747
 1111 CTCACATCAAGCTAAGCTATGTGATTTTGAAGTGCAAAAGGTTCTGGTCTCCTGGTGAA 1052
 748 CCAACATATCATATCTGCTCCCGTATTATTCGTGCTCCAGAACTCATCTTTGGCGCC 807
 1051 CCGAACATATCATATCTGCTCCCGTATTATTCGTGCTCCAGAACTCATCTTTGGTGCA 992
 808 ACAGAGTATACAGCATCCATAGATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 867
 991 ACCGAGTATACAACTTCAATTTGACATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 932
 868 CTGGCCAGCGGTTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAG 927
 931 CTGGTGCAGCCACTGTTTCTGGAGAGAGTGTGTTGACAGCTAGTAGAGATAATCAAG 872
 928 GTTCTTGGTACTCCAACTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTT 987
 871 GTTCTTGGTACTCCAACTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTT 987
 988 AGTGTCCCAAAATCAAGCTCACCTTGGCAAGGTTTTCATAAACGGATGCTTCCA 1047
 811 AAATTTCTCAGATTAAAGCTCATCTTGGCAAGGTTTTCATAAACGGATGCTTCCA 752
 1048 GAAGCAATAGACCTTGCATCTGGCTTCTTCAATATTCACCAAGTCTACGCTGCACTGG 1107
 751 GAAGCAATAGACCTTGCATCTGGCTTCTTCAATATTCACCAAGTCTACGCTGCACTGG 692
 1108 CTCGAAGCATGTGCTCATCTGTTTTCATGAATCTCCGAGAGCAAAAGCTGCTTCCA 1167
 691 CTTGACGCAATGTCACATCTTCTTGTGATGAGCTAGAGAGCCCAATGCAAGCTGCTCCA 632
 1168 AATGGTGTGCTCAATACCGCATGTTTCAATTTCAAAACAGAGTTAGGTGGAGCTTCAATG 1227
 631 AATGGTGTGCTCAATACCGCATGTTTCAATTTCAAAACAGAGTTAGGTGGAGCTTCCA 572
 1228 GAGCTAATCAAGAGGTAATACCTGAGCATGTGAGAGCAAA 1269
 571 GAACATCATCAGAGGCTCATACCGGATCATATCAGAGCGCAA 530

RESULT 4

; Sequence 875, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938, 842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 875
 ; LENGTH: 1143
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-938-842A-875

Query Match 44.0%; Score 710.4; DB 9; Length 1143;
 Best Local Similarity 77.1%; Pred. No. 5.4e-187;

Matches 864; Conservative 0; Mismatches 256; Indels 0; Gaps 0;
 QY 164 TCGATTCTCATAGCAAAATGCTGCAGCTGTGTTATTGAGGGAATACGCTGTACTGTGTC 223
 DB 2 TGGCTGATGATAGGAGATGCTGCTGTGTAGTGTGATGACATGATCAAGTCACTGGTTC 61
 QY 224 ATATCATTTTCCACTACTATAGGAGCAAAACCGGCAACCAAGAGCAGACCATTAGTTACA 283
 DB 62 ATATTATTTCCACCACCAATCGGTGGCAAAATGTTGACCAAAACAGACAAATTAGTTACA 121
 QY 284 TGGCTGAGCGGTTGTTGGAACAGGTTTATTCGGGATGTTTTCAGGCGAAATGCTTGG 343
 DB 122 TGGCGAGCGGTTGTTGGAACAGGTTTATTCGGGATGTTTTCAGGCGAAATGCTTGG 181
 QY 344 AAACCTGGGAAATCAGTACGCTATTAAGAGTCTTCGAAGATCGACGCTATAAAACCGTG 403
 DB 182 AGACTGGGAAACCGTGGCGATTAAGAGGTTTTCGAAGATAGAGATACAGAACCGAG 241
 QY 404 AGTTGCAACTAATCGGACCAATGGATCACCCAAATGTCTATCTCTTGAAGCACTGTTTCT 463
 DB 242 AACTTCAGTTGATGCTGTGATGATCATCCGAATGTGTTGTTTGAAGCATTTGCTTCT 301
 QY 464 TCTCTAACAGAGTATAGATGAGCTTCTCTCAACCTTGTATGAGGATGATGATGAGTAC 523
 DB 302 TTTTCACTACAAAGTAAAGACGAGCTTTCTTGAACCTTGTGTTATGAGGATGATGCT 361
 QY 524 CTTTATACCGGTTTGGAGCACTATAGTGTCTAATCAGAGGATGCAATTTTCTATG 583
 DB 362 GCTGTATCGAGTCTGAAACATATAGTAGTGCAACCAAGAAATGCTTCTTGTCTATG 421
 QY 584 TCAAGCTTTTACATATCAAAATCTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGTG 643
 DB 422 TTAACCTTTACATGATCAGATCTTCCGGGACTTGTTCATATTCACATTCATGTTGCTG 481
 QY 644 TTTGCGACAGAGTATGAAACCAACAAATCTCTTGTGTTGATCCCTTGAGCCCATCAGTTA 703
 DB 482 TTTGTACACAGAGATCTAAAGCCTCAAAATCTTCTGTTGATGCTTCTTACTCAAGTCA 541
 QY 704 AGCTGTGCTATTTGGAAGTCAAAAGTATGCTCAAGGTGAACCAACATATCATATA 763
 DB 542 AAATCTGTGACTTTGGCAGTGGCAACACAGCTGTTAAAGTGAAGCAACATTTCTTACA 601
 QY 764 TCTGCTCCCGTTATTATTCGTGCTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGCAT 823
 DB 602 TCTGCTCAGATTTCTACCGTGCACCGAGCTCATATTTGGTGCACCTGAGTACACAACTT 661
 QY 824 CCATGATATATGCTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 883
 DB 662 CTAATTGATATCTGGTCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 721
 QY 884 TTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGTCTTGTGTTCTCCAA 943
 DB 722 TTTCCCGGAGAAATGCTGTTGATCAGCTGTTGAAATTTAATAAGTCTTGTGTTACCAA 781
 QY 944 CTCGTGAGAAATTCGATGATGAAACCGAACTTACACAGATTTTAGTTCCTCCAAATCA 1003
 DB 782 CTCGAGAAGAAATTCGTTGATGATCCACATTTACACAGATTTTCCAGTTTCCACAGATA 841
 QY 1004 AAGCTCACCTTGGCAAAAGTTTTCATAAAGGATGCTCCAGAGCAATAGACCTTG 1063
 DB 842 AGGCACATCCCTGGCAAAAGTCTTCCACAAAGGATGCTCCCGAGAGCGATGATTTTG 901
 QY 1064 CATCTCGGCTTCTTCAATATTCACCAAGTCTAGCTGCTAGCTGCTGCTGCTGCTGCTGCT 1123
 DB 902 CATCAAGGCTGCTTCAATATCTTCAAGTCTAAGATGCAAGGCTTCAAGCTTGTGTCAC 961
 QY 1124 ATCCGTTTTCATGAACTCCGAGAGCCAAACCGCCGCTCTTCCAAATGTTGCTGCTTAC 1183
 DB 962 ATCCGTTTTCATGAACTCCGAGAGCCAAACCGCCGCTCTTCCAAATGTTGCTGCTTAC 1021
 QY 1184 CGCCATGTTTCAATTTCAAAACAGAGTTAGGTGAGCTTCAATGAGGCTTCAATCAACAGGC 1243
 DB 1022 CGCCTCTCTTCAACTTTCAAAACAGAGTATGCTGATCATCACCTGAACTGGTCAACAGT 1081


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Db 201 TGGCTGATGATAAGGAGATGCCTGCTGTAGTTGATGACATGATCAAGTCACTGGTC 260
QY 224 ATATCATTTCCACTACTATAGGAGGCAAAAACGCGCAACCAAGCAGACCATTTAGTTACA 283
Db 261 ATATTAATTTCCACCAATCGGTGGCAAAATGGTGAACCAAAACAGCAATTAGTTACA 320
QY 284 TGGCTGAGCGGGTGTGTGAACAGGTTCAITCGGGATTTGTTTTCAGGCGAAATGCTTGG 343
Db 321 TGGCGGAGCGAGTGTGTGTGTACAGGCTCGTTGGGATCGTTTCCAAAGCAAAATGTTGG 380
QY 344 AAACCTGGAGATCAGTAGCCATTAATAAGGCTTTGCAAGATCAGCCTATAAAACCGTG 403
Db 381 AGACTGGAGAAACCGTGGCGATAAAGAGGTTTTCGAAGATAGAAGATCAAGAACCGAG 440
QY 404 AGTTGCAACTAAGCGCACCAATGGATCACCCCAATGTCATCTCTTGAAGCACTGTTTCT 463
Db 441 AACTTCAGTTGATGCGGTGATGGATCATCCGAATGTGTTGTTTGAAGCATTTGCTTCT 500
QY 464 TCTCTACAACGAGTAGAGATGAGCTCTTCTCAACCTTGTATGGAGTATGTACCTGAGA 523
Db 501 TTTGACTACAAGTAAGACGAGCTTTCTTGAACCTTGGTATGGAGTATGCCCTGAGA 560
QY 524 CTTTATACCGGGTTTTGAGGCACTATACTAGTTCTAATCAGAGGATGCCAATTTCTATG 583
Db 561 GCTTGTATCGAGTTCTGAACCATATAGTAGTGCAACCAAGAAATGCCCTCTTGTCTATG 620
QY 584 TCAAGCTTTACACATATCAAACTCTTTAGAGGTTTGGCTTACATCCATCTGTTCCGGTG 643
Db 621 TTAACCTTTACATGATCAGATCTTCCGGGACTTGTCTTACATTCACAATGTTGCTGGAG 680
QY 644 TTTGCCACAGAGATGTGAACCAACAAATCTCTTGTGTTGATCCCTTTGACCCATCAGGTTA 703
Db 681 TTTGTACAGAGATCTAAGACCTCAAAATCTCTGTGTGATCTCTTACTCATCAAGTCA 740
QY 704 AGCTGTGTGATTTTGGAGTGCAAAAGTATTTGTCAAAGTGCAACAAACATATCATATA 763
Db 741 AAATCTGTGACTTTGGCAGTGGCAAAACAGCTCGTTAAAGGTGAAGCAACATTTCTTACA 800
QY 764 TCTGCTCCCGTTATATCGTGTCCAGAACTCATCTTTGCGCCACAGAGTATACAGCAT 823
Db 801 TCTGCTCACAAATCTACCGTGCAACCGAGCTCATATTTGTGCGCATGAGTACACAAT 860
QY 824 CCATAGATATATGCTGTGTTGTGTGTAATGCGCAGAGCTTCTTCTTGGCAGCGGTTAT 883
Db 861 CTATTTGATATCTGCTGTGTTGTGTGTTCTTCTGCTGAGCTTCTTCTTGGTCAGCCAT 920
QY 884 TCCAGAGAAATATCAGTTGTATCAGCTTGTGAGATCATAAAGGTTCTTGTACTCCAA 943
Db 921 TTTCCCGAGAAATATGCTGTGGATCAGCTCGTTGAAATTTATAAAGTTCTTGTGTACACCA 980
QY 944 CTGCTGAAGAAATTCGATGTATCAACCCGAACCTACACAGATTTTAGGTTCCCAACATCA 1003
Db 981 CTGGAAGAAATTCGTTGTATGAATCCATTTACACAGATTTTCAAGTTTCCACAGATTA 1040
QY 1004 AAGCTCACCTTGGCAAGAGTTTTTCAATAAAGGATGCTCCAGAGCAATAGACCTTG 1063
Db 1041 AGGCACATCCTGGCAAGATCTTCCACAAAGGATGCCCCAGAAAGGATTTGATTTG 1100
QY 1064 CATCTCGGCTTCTCAATATTCACAAAGTCTACGCTGCACTGCGCTCGAAGCATGTGCTC 1123
Db 1101 CATCAAGGCTGCTTCAATATCTCTCAAGTCTAAGATGCAAGGCTCGAAGCTTGTGCAC 1160
QY 1124 ATCCGTTTTTCAATGAACTCCGAGAGCAACCGCGCTTCCAAATGTTGCTGCTCAATAC 1183
Db 1161 ATCCGTTCTTTGATGAACTCAGAGAACCAACGCTGTTTACCAAATGGAAGCGGCTTTC 1220
QY 1184 CGCCATTTGTTCAATTTCAAAACAAGAGTTAGGTGGAGCTTCAATGGAGCTTAATCAACAGGC 1243
Db 1221 GGCCTCTCTTCAACTTCAAAACAAGAGTAGCTGATCATCACTGAACTGGTCAACAAGT 1280
QY 1244 TAATACCTGAGATGTGAGACGACAAATGAGACAGGATT 1283
Db 1281 TGATTCAGACCATATCAAGAGACAAATTTGGGTTCTTAAGCTT 1320

```

RESULT 7
 US-10-425-114-12807
 ; Sequence 12807, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; NUMBER OF SEQ ID NOS: 2003-04-28
 ; SEQ ID NO 12807
 ; LENGTH: 1726
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 701212714_FLI
 US-10-425-114-12807

Query Match 43.8%; Score 706.2; DB 18; Length 1726;
 Best Local Similarity 76.1%; Pred. No. 1e-185;
 Matches 870; Conservative 0; Mismatches 273; Indels 0; Gaps 0;

QY	141	CGCTTTGAAACGCGCTCGTAATGGATTCTGATAAGGAAATGCTGACAGCTGTTATTGA	200
Db	70	CTCTCTCTCTCCCTCGCCATGGCTAGGATAAGGAGATGCTACCTCTGTCATCAA	129
QY	201	GGGAAATGAGCTGTCTGTCATATCAATTTCCACTATATAGGAGGCAAAACCGCGGA	260
Db	130	TGGGAATGATCCCTAACTGGTCAATCATATCTACAACTATTGGAGGCAAAATGGGA	189
QY	261	ACCAAGCAGACCATTTAGTACATGCTGAGCGGTTGTTGGAACAGGTTCAATTCGGAT	320
Db	190	ACCCAAACAGACTTATAGCTACATGGCAACGCGGTTGAGGAATCGGATCATTTGGAAT	249
QY	321	TGTTTTTCAGGCGAAATGCTTGGAACTGGAAATCAGTAGCCATTAATAAGGCTTTTGCA	380
Db	250	CGTTTTCCAGGCAAAATGCTTGGAACTGGGAGGAGTGGCAATTAATAAGGTTTACA	309
QY	381	AGATCGACGCTATAAAACCGTGAGTTGCAACTAATGCGAACCAATGGATCAACCAATGT	440
Db	310	AGACAGAGATACAGAAATCGTGAACCTGCACTTAATGCGTGTGATGGATCATCCAAATGT	369
QY	441	CATCTCCTTGAAGCACTGTTTCTTCTCTACAACGAGTAGAGATGAGCTCTTCTCCTCAACT	500
Db	370	GATCTCTTGAAGCACTGTTTCTTCTTCAACTCAAGTACAGATGAACTTTTCTCAATTT	429
QY	501	TGTTATGGAGTATGTACCTCGAGACTTTATACCGGGTTTTGAGGCACTATATAGTTCTAA	560
Db	430	GGTATGGAGTATGTTCCAGAGTCCATGTATAGAGTCTTAAGCACTATAGCAATGCTAA	489
QY	561	TCAGAGGATGCCAATTTTCTATGTCAAGCTTTACATATCAATCTTTAGAGGTTTGGC	620
Db	490	TCAAGAAATGCCAATCATCTAGTAAAACTTTATATGTACCAGATTTTCAGGGGTTGGC	549
QY	621	TTACATCCATCTGTTCCCGGTTTGGCCACAGAGATGTGAACCAACCAAACTCTTCTGTT	680
Db	550	TTACATCCACACTGGTCCCAAAAGTTTGGCCACAGAGATTTGAAGCCCTCAAAATATCTGTT	609
QY	681	TGATCCCTTGACCCATCAGGTTAAGCTGTGTGATTTTGGAAAGTGAAGGATTTTGGTCAA	740
Db	610	GGATCTCTTACACACCAAGTGAAGTATGTGATTTTGGAAAGTGAAGGTTCTAGTGA	669
QY	741	AGGTGAACCAACATATCATATATCTGCTCCCGTTATATATGCTGCTCCAGAACTCATCTTT	800

<p> RESULT 9 US-09-854-731-15 ; Sequence 15, Application US/09854731 ; Patent No. US20020120949A1 ; GENERAL INFORMATION: ; APPLICANT: Allen, Steve ; APPLICANT: Lee, Jian Ming ; TITLE OF INVENTION: Plant Protein Kinases ; FILE REFERENCE: BB-1171 ; CURRENT APPLICATION NUMBER: US/09/854,731 ; PRIOR FILING DATE: 2001-05-14 ; PRIOR APPLICATION NUMBER: 60/092,438 ; PRIOR FILING DATE: July 10, 1998 ; NUMBER OF SEQ ID NOS: 23 ; SOFTWARE: Microsoft Office 97 ; SEQ ID NO 15 ; LENGTH: 1673 ; TYPE: DNA ; ORGANISM: Triticum aestivum ; FEATURE: ; NAME/KEY: unsure ; LOCATION: (1349) ; US-09-854-731-15 </p>									
<p> Query Match 43.5%; Score 701.6; DB 9; Length 1673; Best Local Similarity 74.7%; Pred. No. 1.9e-184; Matches 881; Conservative 0; Mismatches 299; Indels 0; Gaps 0; </p>									
QY	98	AGCCTCATGCTCTGTGCTCGCCGCTGCGAGCTTCACGACGCGCAGCGCTTTTGAACGCGGTC	157						
DB	48	AGCATCGGCGCGCGCGCGGAGCCGATGCTGCTCGACGAGCAGCCCCCACCAGCAGTCG	107						
QY	158	CTGAATTGAAATCTGTAAGGAATATGTCGACGCTGTTATGAGGAAATGACGCTGTTA	217						
DB	108	CTGCGAGAAGAAGCAGCAGATGCGGAGCGCGCTATGCGAGGGAAGCAGCGCCATGA	167						
QY	218	CTGGTCATATCATTTCCACTACTATAGGAGGCAAAACCGCGAACCAAGCAGACCATTA	277						
DB	168	CCGGTCACATCATCTCCACCACCATCGCGGCAAGAACGCGAGGCCAAGCAGACGATTA	227						
QY	278	GTACATGCTGAGCGGGTGTGGAAACAGGTTTCATTGGGATGTTTTCAGGCGAAAT	337						
DB	228	GCTACATGGGAGCGGTTGTGGGCATGTTTCGTTTGGCATCGTCTTCAGGCTAAT	287						
QY	338	GCTTGAAATCGAGAAATCAGTAGCCATTAAGGCTTTGGAAGATCGACGCTATAAA	397						
DB	288	GCCTGGAACCGGGAGATGTTGGGCATTAAGAGGTTACTGCGAGGACAGACGGTACAAG	347						
QY	398	ACGCTGAGTTGCAACTAATCGCAACCAATGGATCACCAATGTCATCTCCTTGAACACT	457						
DB	348	ACCGTGAGCTGAGCTTATGCTGATGATGATGATGATGATGATGATGATGATGATGATG	407						
QY	458	GTTCCTCTCTACACGAGTAGAGTAGCTCTTCTCTCAACCTTGTATGAGATATGTAC	517						
DB	408	GCTTCTCTCAACCAAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGTAGAGT	467						
QY	518	CTGAGACTTTATACCGGGTTTGGAGCATACTAGTATGATGATGATGATGATGATGATG	577						
DB	468	CGGAGAGCGCTATACCGGGTCTTAAAGCATACTAGTATGATGATGATGATGATGATG	527						
QY	578	TCTATGTCAGCTTTACACATATCAATCTTTAGAGGTTTGGCTTACATCATCTGTTTC	637						
DB	528	TCTATGTCAGCTTTACATGATACAGCTTTTAAAGGCTAGCTTATGTTTCACTGTTTC	587						
QY	638	CCGGTGTTCGCCACAGAGATGTGAACCAACAAATCTCTTGGTGTGATCCCTTGAACCATC	697						
DB	588	CAGGAGTTTCGCCACAGGATGTGAACCAACAAATCTCTTGGTGTGATCCCTTGAACCATC	647						
QY	698	AGTTAAGCTGTGATTTTGGAAAGTGAAGTATGTTGTTGTTGTTGTTGTTGTTGTTGTTG	757						
DB	648	AAGTCAGATCTGTGACTTTGGAAAGTGAAGTATGTTGTTGTTGTTGTTGTTGTTGTTG	707						

QY	758	CATATATCTGCTCCGTTATTTATCTGCTCCAGAACTCATCTTTGGCGCCACAGAGTATA	817						
DB	708	CATACATATCTCTCGTACTATCTGCTCTCTGAGCTCATATTTGGTGAACCTGATATA	767						
QY	818	CAGCATCCATAGATATATGTTCTGCTGTTGTGTATGCGCAGAGCTTCTTCTTGGCCAGC	877						
DB	768	CAACTTCAATAGACATATGTTCTGCTGAGTGTGTTCTTGACAGAGCTACTTCTTGGTCAGC	827						
QY	878	CGTTATTTCCAGGAGAAATTCAGTTGATCAGCTGTGGAGATCATAAAGGTTCTTGTA	937						
DB	828	CTCTGTTTCCAGGAGAGACTGCGGTTGATCAGCTAGTGGAGATTATCAAGGTTCTTGTA	887						
QY	938	CTCCAACTCGTGAAGAAATTCGATGTATGAAACCCGAACTACACAGATTTTAGGTTCCAC	997						
DB	888	CTCCAACTCGTGAAGAAATTCGATGTATGAAACCCGAACTACACAGATTTTAGGTTCCAC	947						
QY	998	AAATCAAAGCTCACCTTGGCAAGGTTTTCATAAACCAGATGCTCCAGAAAGCAATAG	1057						
DB	948	AGATTAAAGGCTCATCTTGGCAAGATTTTCCAAAGAGAAATGCCCGCTGAAGCTATAG	1007						
QY	1058	ACCTTGATCTCGGCTTCTCAATATTCACCAAGTCTAGCTGCACTGCGCTCGAGGAT	1117						
DB	1008	ATCTTGCTCCCGCTTCTCCAGATATTCACCAAACTACGTTGCACTGCTCTTGATGCA	1067						
QY	1118	GTGCTCATCCGTTTTCATGAACCTCCGAGAGCAAAACCGCGCTCTTCCAAATGGTCGTC	1177						
DB	1068	GTGCAATTTCTTCTTGTGATGAGCTACGTGCGGAGTGCAGCTTGCAGATGGCGGCC	1127						
QY	1178	CATTACCGCATTTGTTCAATTTCAAACAAGATTTAGTGGAGCTTCAATGGAGCTAATCA	1237						
DB	1128	CATTCCCTCTCTGTTTCACTTCAAACCTGAACCTAGCAAGCGCTCTCCAGAGCTCATCA	1187						
QY	1238	ACAGGCTAATCTGAGCATGTGAGACGACCAATGAGCAC	1277						
DB	1188	ACAGGCTTGTTCGGAACATGTTCCGACGCAAAATGGCCC	1227						

RESULT 10
 US-10-424-599-67987
 ; Sequence 67987, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 67987
 ; LENGTH: 1881
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_32405C.1
 US-10-424-599-67987

<p> Query Match 43.4%; Score 699.8; DB 18; Length 1881; Best Local Similarity 75.8%; Pred. No. 6.5e-184; Matches 866; Conservative 0; Mismatches 277; Indels 0; Gaps 0; </p>									
QY	141	CGTTTGAACCGCGCTCTGAAATTTGATTTGATTTCTGATAGGAAATGCTGCGAGCTTTATTGA	200						
DB	112	CTCA	171						
QY	201	GGGAATGAGCTGTTTACTGTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	260						
DB	172	TGGGAATGAGCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	231						
QY	261	ACCAAGAGAGACCATTTAGTTTACATGCTGAGCGGGTGTGGAAACAGGTTTCATTCGGGAT	320						


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Db 232 ACCCAACAGACTATTAGTTTACATGCGAAGCGGTTGTAGAACTGGGATCATTTGGAAAT 291
Qy 321 TGTCTTTTTCAGGGAAATGCTTGGAAATCAGTAGGCAATTAAGAAAGTCTTGCA 380
Db 292 TGTCTTTTTCAGGGCAAAATGCTTGGAAATCAGTAGGCAATTAAGAAAGTCTTGCA 351
Qy 381 AGATGACGCTATAAAACCGTGGAGTTGCAACTAATGCGAACCAATGAGTACCCAAATGT 440
Db 352 AGACAGAGATACAAGAAATCGTGAACACTACAGTTAATGCGTGTGATGAGTATCAATCAATGT 411
Qy 441 CATCTCTTGAAGCACTGTTCTCTCTCAACAGAGTAGAGTACGCTCTTCTCAACT 500
Db 412 GATCTCTTGAAGCAATGTTCTCTCTCAACAGTACTGATGAACTTTTCTTAATTT 471
Qy 501 TGTATGAGATGTACCTGAGACTTTATAACCGGTTTGTAGGCACTATACCTAGTTCTAA 560
Db 472 GGTGATGAGATGTATGTCAGAGTCCATGTATAGAGTCTTAAAGCACTACAGCAATGCTAA 531
Qy 561 TCAGAGGATGCCAATTTCTATGTCAAGCTTTACACATATCAAAATCTTTAGAGTTTGGC 620
Db 532 TCAAGAAATGCCATATCTACGTTAAACTTTATATATGACCAAGATTTTCAGGGGTTTGGC 591
Qy 621 TTACATCCATCTGTTCCCGGTTTGGCCACAGAGATGTGAACCAACCAAAATCTCTTGGT 680
Db 592 TTATATCCACACTGTTCCCAAGTTTGGCCACAGAGATTTGAAGCCTCAAAATATATCTGT 651
Qy 681 TGAATCCCTTGACCCATCAGGTTAAGCTGTGTGATTTTGAAGTGAAGAAATTTGGTCAA 740
Db 652 GGATCCTCTTACACACCAAGTGAAGCTATGTGACTTTTGAAGTGCNAAGTTCTAGTCA 711
Qy 741 AGGTGAACCAACATATATATATCTGCTCCCGTTATATCTGTCTCCAGAACTCATCTT 800
Db 712 AGGTGAAGCTAATATATATATATATGTTTCAAGTTCTATCGAGCACCAGAACTCATAT 771
Qy 801 TGGCCGCCACAGAGTATACAGATCCATAGATATGCTCTGCTGCTGTGTGACTGGCAGA 860
Db 772 TGGGCCCACAGAGTATACAGATTTCAATTTGATTTTGGTCAAGCTGTGTCTTGTCTGA 831
Qy 861 GCTTCTCTTGGCCAGCGGTTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGAT 920
Db 832 ACTTCTTTTGGCCAGCCATATTTCCCTGGCGAAATTCAGTAGACAGCTTGTATATAT 891
Qy 921 CATAAAGGTTCTTGATCTTCAACTCGTGAAGAAATTCAGTATGATGAACCCGAACTACAC 980
Db 892 TATAAAGGTTCTTGCGACGCCCACTCGAGAGGAAGTACGCTGTATGAATCCCAATTA 951
Qy 981 AGATTTTGGTTCCCAAAATCAAAAGCTCACCTTGGCAGAGGTTTTCATAAACGGAT 1040
Db 952 TGACTTTTGGTTTCTCAGATAAAAGCACCCATGGCAGAGATATTTCCAAAGAT 1011
Qy 1041 GCCTCCAGAGCAATAGACCTTGCATCTCGGCTTCTTCAATATTCACCAAGTCTACGCTG 1100
Db 1012 GCCTCCGAGAGCTATGTATCTGATCTCGGCTTGTGATATCTCCCAAGTCTCCGCTG 1071
Qy 1101 CACTGCGTCCGAGCATGTCTCATCTCGTTTTCATGAAGTCCGAGAGCCAAAGCCCG 1160
Db 1072 CACTGCACTTGAAGCATGTGCACATCTCTTCTTGTATGAACCTTGTGAACCCAGCTCG 1131
Qy 1161 TCTTCCAAATGGTCTGTCATTAACCCCATTTGTTCAATTTCAAGAGATTTAGTGGAGC 1220
Db 1132 CCTGCAAAATGGTCCCAATTTCCCTCTTATTTAACTTCAACAGAGAAATATCTGGAGC 1191
Qy 1221 TTCAATGAGCTTAATCAACAGGCTAATACCTGAGCATGTGAGACGACAAATGAGCAGG 1280
Db 1192 ATCTCCGAGCTTGTAAATAGTTGATACCTGACCATGTGAAGCGGCAATGGGCTACA 1251
Qy 1281 ATT 1283
Db 1252 ATT 1254
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RESULT 11

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US-10-424-599-67989
; Sequence 67989, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 67989
; LENGTH: 1744
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_32407C.1
US-10-424-599-67989
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Query Match 43.3%; Score 699.2; DB 18; Length 1744;
Best Local Similarity 77.5%; Pred. No. 9.2e-184;
Matches 859; Conservative 0; Mismatches 248; Indels 1; Gaps 1;
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Qy 164 TGGATTTCTGATAAGGAAATGTCGAGCTGTTATTGAGGGAATGACGCTGTACTGTGTC 223
Db 123 TGGCTGAGATTAAGAGATGCTTCTCTGTGTCACCAATGGCGATGATCTCTCACTGGCC 182
Qy 224 ATATCATTTTCCACTACTACTAGAGGCAAAACCGGGAACCAAGCAGACCATATTAGTTACA 283
Db 183 ACATCATATCTACAACTATTGGAGGCAAAATGGGGAACCCCAACAGACTATTAGTTACA 242
Qy 284 TGGCTGAGCGGTTGTTGGACAGGTTTCATTCGGGATGTTTTCAGCGGAATGCTTGG 343
Db 243 TGGCTGAAACGGGTTGTAGGAACTGGATCATTTGGAAATTTGTTTCCAGGCAAAATGTTGG 302
Qy 344 AAACCTGGAAGATCACTAGTACCCATTAAAAAGGCTTTCGAAGATCGAGCTATAAAAACCGTG 403
Db 303 AAACCTGGGAGAGTGGCCATTAAAAAGGTTTTCAGAGACAGAGATACAGAATCGTG 362
Qy 404 AGTTGCAACTAATGCGACCAATGGAATCAACCAATGTCATCTCTTGAAGCACTGTTTCT 463
Db 363 AACTACAGTTAATGCTGTTTGGATCATCCAAATGTCATCTCTCTGAAGCACTGTTTCT 422
Qy 464 TCTCTACAAACGAGTAGAGTACGCTCTTCTCAACCTTGTATGAGTATGTACCTGAGA 523
Db 423 TTTCAACTACAAAGTACAGATGAGCTTTTCTTAATTTGGTGAATGATGTTCCAGAGT 482
Qy 524 CTTTATACCGGTTTGTAGGCACTATACCTAGTCTTAATCAGAGGATGCCAATTTTCTATG 583
Db 483 CCATGTATAGATCATTTAAGCACTATATACTAATGCTAATCAAGAGATGCCAATCATCTATG 542
Qy 584 TCAAGCTTTTACATATCAAAATCTTTAGAGTTTGGCTTATCATCATCTGTTCCCGGTG 643
Db 543 TAAACCTTTACATGTCAGATTTTTCAGGGAATGGCTTATATCCACACTGTTCCCAAG 602
Qy 644 TTTGCCACAGAGATGTGNAACCAAAATCTTCTGGTTGATCCCTTGGACCCATCAGTTA 703
Db 603 TTTGCCACAGAGATGTGAAGCCTCAAAATATATCTGGTGGATCTCTTACACACCAAGTGA 662
Qy 704 AGCTGTGTGATTTTGGAGTCAAAAGTATTGGTCAAAAGGTGAACCAACATATCATATA 763
Db 663 AGCTATGTGATTTTGGAGTGCAAAAGTCTAGTAAAAGGTGAAGCTAATATATCATACA 722
Qy 764 TCTGCTCCCGTTATATCTGCTCCAGAACTCATCTTTTGGCGCCACAGAGTATACAGCAT 823
Db 723 TATGTTACAGATTTCTATCGCGCTCCAGAACTTATATTTTGGCGCCACAGAGTATACAAGT 782
Qy 824 CCATAGATATATGTTCTGCTGGTTGTGTACTGGCAGAGCTTCTTCTTGGCCAGCGTTAT 883
Db 783 CAATTGATATTGTTGCTGCTGCTGTGCTTCTTGTGAACTTTCTTTTGGGCCAGCCATTAT 842
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QY 884 TTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCCAA 943
 DB 843 TTCTCGCG-AAAATGAGTAGACAGCTTGGTCATATTAAGGTTGGCAGACCCA 901
 QY 944 CTCGTGAAGAAATTCGATGATGAACCCGAACTACACAGATTTAGGTTCCACAAATCA 1003
 DB 902 CTCGAGAGGAAGTACGCTGTATGAATCCCAATTAACAATGACTTTGTAGGTTCCACAGATAA 961
 QY 1004 AAGCTCACCTTGGCAGAGGTTTTCATTAACGGATGCTCCAGAAAGCAATAGACTTG 1063
 DB 962 AAGCACACCCATGGCAAGATATTCACAAAGATGCTCCAGAAAGCAATTTGATCTTG 1021
 QY 1064 CATCTCGGCTTCTCAATATTCACCAAGTCTACGCTGCACTGGCTCGAAGCATGTGCTC 1123
 DB 1022 CATCCCGCTTTTGCATATCTCCCAAGTCTCGATGCACTGGCTTGAAGCATGTGCTC 1081
 QY 1124 ATCCGTTTTTCAATGAACCTCCGAGAGCCAAACCGCTCTTCCAAATGGTCTGCATTAAC 1183
 DB 1082 ATCCCTTTTGTGATGAATTCGAGAACCCCAATGCTCGCTGCCAAATGGTCTGCATTTTC 1141
 QY 1184 CGCATTTGTTCAATTTCAACAAAGAGTTAGTGGAGCTTCAATGGAGCTTAATCAACAGGC 1243
 DB 1142 CTCCTTTATTTAACTTCAAGCAGGAATTTATCCGAAGCTTCCAGAGCTTGTGAACAAAG 1201
 QY 1244 TAATACCTGAGCATGTGAGACGACAAAT 1271
 DB 1202 TGATACCTGACCATGAAGCGGCAAT 1229

RESULT 12

US-10-424-599-124786
 ; Sequence 124786, Application US/10424599
 ; Publication No. US20040031072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa Thomas J
 ; APPLICANT: Kovalic David K
 ; APPLICANT: Zhou Yihua
 ; APPLICANT: Cao Yongwei
 ; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53223)B
 ; CURRENT APPLICATION NUMBER: US/10/424,599
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 285684
 ; SEQ ID NO 124786
 ; LENGTH: 2519
 ; TYPE: DNA
 ; ORGANISM: Glycine max
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT3847_83691C.1
 US-10-424-599-124786

Query Match 43.3%; Score 698.2; DB 18; Length 2519;
 Best Local Similarity 76.7%; Pred. No. 2.2e-183;
 Matches 892; Conservative 0; Mismatches 268; Indels 3; Gaps 3;
 QY 115 CCSCCGCTGACGCTTACAGCGGAGCGCTTTGAAACCGCGCTCCTGAAATGGATTTCTGAT 174
 DB 739 CCSCCGCAGTGTGAGCGGCAACCGAAGTTCTCTCGCGGAGCTCCGATATGGAGACCGAT 798
 QY 175 AAGGAATGCTCAGCTGTTATTGAGGAAATGACGCT-GTTACTGGTCAATATCATTTTC 233
 DB 799 AAGGATGTCAGCTACTGTGTCATTGAGGGGAATGATGACGTTACTTGGCCACATAATCTC 858
 QY 234 CACTACTATAGGAGGCAAAACCGCAACCAAGACGACCAATTTAGTTACATGGCTGAGCG 293
 DB 859 CACCACAAATTTGAGGCAAAATTTGGGAACCTTAACAGACCATCAGTTACATGCGAGAACG 918
 QY 294 GGTGTTGGAACAGGTTTCATTCGGGATTTGTTTTTCAGGCGAAATGCTTGGAAATCTG-GAG 352
 DB 919 TGTGTTGGCACTGGATCAATTTGGAGTTGTTTTCCAGGCAAGTGTCTTGGAGACTCGGAG 978

RESULT 13
 US-10-292-408-21
 ; Sequence 21, Application US/10292408
 ; Publication No. US20030182692A1
 ; GENERAL INFORMATION:
 ; APPLICANT: VAN THIELEN, NOCHA
 ; APPLICANT: DA COSTA E SILVA, OSWALDO
 ; APPLICANT: CHEN, RUOYING

QY 353 AATCAGTAGCCATTAAAAAGGTTCTTCAAGATCGAGCTATATAAAACCGTAGTTTCAAC 412
 DB 979 AGGCAGTGGCTATTAATAAGGTTCTTGCAGACAGGCGATACAAAATCGAATTCAGT 1038
 QY 413 TAATGCGCAATGAGTCAACCCAAATGTCATCTCTTGAAGCACTGTTTCTTCTTACAA 472
 DB 1039 TAATGCGCTTAATGAGTCAACCCAAATCTAACTTACATGAAGCACTTTTAAATTTCTCAT 1098
 QY 473 CGAGTAGAGAT-GAGCTCTTCTCAACCTTGTATGAGAGTATGTACCTCAGACTTTTATAC 531
 DB 1099 CAAGCAAGATCCAACTTTTCTAAACCTTGTAAATGAGATATGTCCCTGAGTCAATCAAC 1158
 QY 532 CGGGTTTTGAGGCACTATCTAGTTTCTAATCAGAGGATGCCAAATTTTCTATGTCAAGCTT 591
 DB 1159 CGAATTTAAACCATTTACACTACTATTAACAGAGAGATGCTCTCATCTACGTGAAGCTG 1218
 QY 592 TACACATATCAAACTTTTAGAGGTTTGGCTTACATCCATACCTGTTCCCGGTGTTTGGCAC 651
 DB 1219 TATACATATCAAACTTTCAGGGGATTTAGCATATATCCATACCGCTTGGAGTTTGGCAT 1278
 QY 652 AGAGATGTGAACCAACCAAAATCTCTTGGTTGATCCCTGACCCCATCAGGTTAAGCTGTGT 711
 DB 1279 AGGATGTAAAGCTTCAAAATCTTTTGGTTTCTTCTTACTCACCAGTTAAGCTATGT 1338
 QY 712 GATTTTGAAGTGCAAAAGTATTTGGTCAAAAGGTGAACCAACATATCATATATCTCTCC 771
 DB 1339 GATTTTGGAGTGCCTCAAGCTTCTTGGTCAAGGTTGAATCAACATTTTATACATATGTCA 1398
 QY 772 CGTTATTTCTGCTCCAGAACTCATCTTTTGGCGCCACAGGTATACAGATTCATATAGAT 831
 DB 1399 CGTTACTATCGGCTCCAGAACTTAATTTGGTGAACCTGAAATACACACCTTCTATTGAT 1458
 QY 832 ATATGCTCTGCTGGTTGTGCTAGTGGCAGAGCTTCTTCTTGGCGAGCGTTATTTCCAGGA 891
 DB 1459 ATCTGCTCAGCTGGTTGTGTTCTTGTCTGCTGAACTTCTTCTAGGACAGCAATTTGTTCTCTGGA 1518
 QY 892 GAAATTCAGTTGATCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCCAACTCGTGAA 951
 DB 1519 GAAATCAGTGGAGCCAACTTGTGGAAATTAATTAAGTTCTTGGTACTCGACTCGGAG 1578
 QY 952 GAAATTCGATGATGAACCCGAACTACACAGATTTTAGTTTCCCAAAATCAAAGCTCAC 1011
 DB 1579 GAAATCCGTTGATGAACCCAAATTAACAGATTTTAGATTTCCCTCAGATTTAAAGCTCAT 1638
 QY 1012 CTTTGGCAAGAGGTTTTCATAAACGATGCGCTCCAGAGCAATAGACCTTGCATCTCGG 1071
 DB 1639 CTTTGGCAAGAGGTTTTCACAAAGCGAATGCTCTGGAAGCAATGACCTTGCATCAAGG 1698
 QY 1072 CTTCTTCAATATTCACAAAGTCTACGCTGCACTGCGCTCGAAGCATGTGCTCATCCGTTT 1131
 DB 1699 CTTCTCAATATTCACCTAGTCTACGCTGCACTGCGCTGGAAGCATGTGCACATCTTTTC 1758
 QY 1132 TTCAATGAACTCGAGAGCCAAACGCGCTTTCCAAATGGTGTGCTGCATTAACGCCATTG 1191
 DB 1759 TTTGATGAGCTTCGCGAGCCAAATGCGCTTCTTCTTAATGGCCATCCACTCGCCCACTT 1818
 QY 1192 TTTCAATTTCAACAAAGGTTTAGTGGAGCTTCAATGAGCTAATCAACAGGCTAATACCT 1251
 DB 1819 TTTCACTTCAACAGAGGTTTAGTGGAGCATCACCTGAACTGATCAATAGGCTCATCCCCA 1878
 QY 1252 GAGCATGTGAGACGACAAATGAG 1274
 DB 1879 GAGCATATTAGGCGGAGATGGG 1901

;; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED POLYPEPTIDES AND METHODS
;; FILE REFERENCE: 16313-0178
;; CURRENT APPLICATION NUMBER: US/10/292,408
;; CURRENT FILING DATE: 2002-11-12
;; PRIOR APPLICATION NUMBER: 60/346,096
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 51
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 21
;; LENGTH: 1499
;; TYPE: DNA
;; ORGANISM: Glycine max
US-10-292-408-21

Query Match 43.0%; Score 693.4; DB 16; Length 1499;
Best Local Similarity 76.2%; Pred. No. 3.5e-182;
Matches 853; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

QY 152 GCCGCTCGAATTGGAATTCGTGTAAGGAATGTCTGACGCTGTTATGTGGGAAATGACG 211
DB 153 GCGGCTCCGACCGCGCACGAAAGGAATGTCTGCTCGCAGATGGTAATGATG 212
QY 212 CTGTTACTGCTCATATCTTCCACTATATAGGAGGCAAAACGCGAACCAAGACAGA 271
DB 213 CACTCACTGGTCACTAATCTCAACCAATTTGCGAGGCAAAATGCGGAACCTAAACAAA 272
QY 272 CCATTAGTTACATGGTCGCGGTTGTTGGAACAGGTTCAATTCGGGATTTGTTTCCAGG 331
DB 273 CCATCAGTTACATGGCGCAACGTTGTTGGCACTGGATCAATTTGCCATTTGTTTCCAGG 332
QY 332 CGAATGCTTGAACATGAGAGATCAGTAGCCATTAATAAGTCTTTCGAAGATCGACGCT 391
DB 333 CGAAGTCTTGGAGACTGCGGAGGAGTGGCTATATAAGAGGTTCTTGCAGGACAGCGAT 392
QY 392 ATAAAAACGTCAGTTGCAACTAATGCGACCAATGATCACCACCAATGTCTCTCTTGA 451
DB 393 ACAAATCGTGAACGTTGTAATGCGGCTGATGGATCACCACCAATATAATTTCTTGA 452
QY 452 AGCACTGTTTCTCTACACGAGTAGAGATGAGCTCTTCTCAACCTTGTATGAGAT 511
DB 453 GTAACATTTCTCTACACAGTAGAGATGAACTTTTCTGAACTTGTGATGGAAT 512
QY 512 ATGTACTGAGACTTTATACCGGTTTGGAGCACTATACATGTTCTAATCAGAGATGC 571
DB 513 ATGTCCCTGAGACGATCTTCCGTTTATAAAGCACTACAGTAGCATGAAACAGAGAAATGC 572
QY 572 CAATTTCTATGCTCAAGCTTTACACATATCAATCTTTAGAGGTTGGCTTACATCCATA 631
DB 573 CCTAATCTATGTGAATTTATATACATATCAATCTTTAGGGGACTGGCGTATATCCATA 632
QY 632 CTGTTCCCGGTTTGGCCACAGAGATGTGAACCAACCAAAATCTTGTGTTGATCCCTTGA 691
DB 633 CTGTACCAGGAATCTGCCATAGGATTTGAGCCCTCAAAATCTTTGTTGATCACTCA 692
QY 692 CCCATCAGGTTAAGCTGTGTGATTTTGGAAAGTGCAAAAGTATTTGTCAAAGGTGAACCA 751
DB 693 CACACCAAGTCAAGCTGTGTGATTTTGGAGTGCAAAAGTCTCTGTGGAGGTTGAATCAA 752
QY 752 ACATATCATATATCTCTCCGTTTATATCGTCTCCAGAACTCATCTTTGGCGCCACAG 811
DB 753 ACATTTTACATATATGTTCAAGGTTACTATCGTGGCCCGAGAGCTAATATTTGGTGGCGG 812
QY 812 AGTATACAGCATCCATAGATATATGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 871
DB 813 AATACACAACCTTCTGTTGATTTTGGTCCGCTGTTGTTGTTGTTGTTGTTGTTGTTG 872
QY 872 GCCAGCGTTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGGAGATCAATAAGGTTTC 931
DB 873 GCCAGCTTTGTTCCAGGAGAAATCAGTTTGACCAACTCGTGGAAATTAATCAAGATTC 932
QY 932 TTGGTACTCCAACTCGTGAAGAAATTCGATGTATGAACCCGAACTACACAGATTTAGGT 991

RESULT 14

US-10-424-599-26109
; Sequence 26109, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 26109
; LENGTH: 1553
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_123578C.1
US-10-424-599-26109

Query Match 43.0%; Score 693.4; DB 18; Length 1553;
Best Local Similarity 76.2%; Pred. No. 3.6e-182;
Matches 853; Conservative 0; Mismatches 266; Indels 0; Gaps 0;

QY 152 GCCGCTCGAATTGGAATTCGTGATAAGGAATGTCTGACGCTGTTATTGAGGGAATGACG 211
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QY 452 AGCACTGTTTCTCTACACAGGATAGAGATGAGCTCTTCTCAACCTTGTATGAGAT 511
DB 514 GTAACATTTCTTCTCTACAAAGAGTAGAGTAACATTTTCTGAACTTGGTATGGAAT 573

Db	569	GAGAGCCACATGGCGGTTGCCAAATGGAGGGCCATTCTCCACTGTTCAACTTTAAAC	510
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Db	509	AGGAAGTACCAATGCTCCCGGAGCTCATCAACAGGCTGATCCGAGACCATGCTAGGC	450
Qy	1265	GACA	1268
Db	449	GGCA	446

Search completed: June 24, 2005, 08:33:20
Job time : 1743.22 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 10:16:02 ; Search time 8015.32 Seconds
(without alignment)
7664.793 Million cell updates/sec

Title: X99696

Perfect score: 1614

Sequence: 1 AAGCAAGACAGAGGAAAAA.....CCAAAAA.....1614

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1293.2	80.1	1461	3	CNS0AB1V	BX817800 Arabidops
2	1284.6	79.6	1409	3	CNS0AB1V	BX815323 Arabidops
3	713.2	44.2	1197	9	CL957492	CL957492 OsIFCC000
4	676	41.9	1745	3	AY106255	AY106255 Zea mays
5	665	41.2	1666	3	AY104068	AY104068 Zea mays
6	635.4	39.4	924	7	CK266410	CK266410 EST172488
7	603.4	37.4	920	1	AV827407	AV827407 AV827407
8	584.4	36.2	1967	3	AY103545	AY103545 Zea mays
9	581.8	36.0	932	7	CV290871	CV290871 aof01-15m
10	576.6	35.7	2295	9	CL964803	CL964803 OsIFCC011
11	575	35.6	910	7	CK290108	CK290108 EST1752830
12	574	35.6	1638	3	CNS09XSF	BX81446 Arabidops
13	572.2	35.5	591	1	AV831097	AV831097 AV831097
14	572	35.4	829	6	CB971865	CB971865 CAB10006
15	551.4	34.2	1752	3	AY108486	AY108486 Zea mays
16	551.2	34.2	963	7	CK286429	CK286429 EST749151
17	549.2	34.0	952	7	CK289285	CK289285 EST752007
18	547.4	33.9	1275	9	CL963186	CL963186 OsIFCC008
19	547	33.9	944	7	CK290066	CK290066 EST752788
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26	526	32.6	1870	3	CNS0ADOL	BX813745 Arabidops
27	524.2	32.5	821	6	CB894470	CB894470 EST647262
28	521.6	32.3	910	7	CK273024	CK273024 EST719102
29	515.2	31.9	926	7	CK269187	CK269187 EST715265
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33	505	31.3	730	7	CV051935	CV051935 EST_11383
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41	491.2	30.4	841	7	CF515381	CF515381 CAP0001_I
42	491	30.4	868	7	CK287818	CK287818 EST750570
43	488	30.2	704	7	CNS08425	CNS08425 O30121ABL
44	486.4	30.1	1810	3	CNS0ADRT	BX814445 Arabidops
45	485.4	30.1	840	4	BM779604	BM779604 EST590180

ALIGNMENTS

RESULT 1
LOCUS CNS0AB1V 1461 bp mRNA linear HTC 06-FEB-2004
DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLSL42ZC04 of Silique of strain col-0 of Arabidopsis thaliana (thale cress).
ACCESSION BX817800
VERSION BX817800.1 GI:42471112
KEYWORDS HTC; GSLT cDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE Castelli,V., Aury,J.M., Jaillon,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scarpelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,J. and Salanoubat,M.
TITLE Whole Genome Sequence Comparisons and 'Full-Length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1461)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequençage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Web : www.genoscope.cns.fr)
COMMENT The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URGV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/banque_Projet_EF/Full length http://www.genoscope.cns.fr/cgi-bin/ggb?source=Arabidopsis. Location/Qualifiers 1..1461 /organism="Arabidopsis thaliana" /mol_type="mRNA" /strain="Col-0" /db_xref="taxon:3702"

FEATURES
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Matches 1295; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
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QY	697 CAGGTTAAGCTGTGATTTTGAAGTGCAAAAGTATGTCACAAAGTGAAACCAACATA 756
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QY	817 ACAGCATCCATAGATATATGCTGCTGTTGTTGTTACTGGCAGAGCTTCTTCTGGCCAG 876
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QY	937 ACTCCCACTCGTGAAGAAATTCGATGTATGAACCCGAACCTACACAGATTTTAGGTTCCCA 996
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QY	997 CAAATCAAAGCTCACCCCTTGGCACAAGGTTTTTTCATAACCGATGCTCTCCAGAGCAATA 1056
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Db	1261 AAACCTGTGCATCTCGAAGAGAAAGAGGAGAAAAGCAG 1298
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CNS0ABFT	1409 bp mRNA linear HTC 06-FEB-2004
LOCUS	Arabidopsis thaliana Full-length cDNA Complete sequence from clone
DEFINITION	GSLT5S1ZG09 of Adult vegetative tissue of strain col-0 of Arabidopsis thaliana (thale cress).
ACCESSION	EX815323
VERSION	1 GI:42471412
KEYWORDS	HTC; GSLT cDNA.
SOURCE	Arabidopsis thaliana (thale cress)
ORGANISM	Arabidopsis thaliana
REFERENCE	
1 (bases 1 to 1409)	
Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M. 1999. The Arabidopsis genome: A combined approach to evaluate and improve the Arabidopsis genome annotation. Genome 42: 1409-1419.	
TITLE	
A Combined Approach to Evaluate and Improve the Arabidopsis Genome Annotation	
JOURNAL	
Unpublished	
AUTHORS	
2 (bases 1 to 1409)	
Genoscope.	
Direct Submission	
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)	
COMMENT	
The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full length	
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QY	164	TGGATTCTGATAAGGAAATGCTGCAGCTGTTATTGAGGGAATGACGCTGTTACTGGTC	223				
DB	121	TGGATTCTGATAAGGAAATGCTGCAGCTGTTATTGAGGGAATGACGCTGTTACTGGTC	180				
QY	224	ATATCATTTCCACTACTATAGAGGCAAAACCGGCAACCAAGCAGACCATAGTTACA	283				
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QY	404	AGTTGCAACTAATGCGACCAATGATGATCAACCAATGTCATCTCTGAAGCACTGTTCT	463				
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QY	1304	GCATGCTCTGAAGAGAAAGAGGAGAAAGCAG	1334				
DB	1261	GCATGCTCTGAAGAGAAAGAGGAGAAAGCAG	1291				
RESULT 3							
LOCUS		CL957492					
DEFINITION		OBIFCC00689 Oryza sativa Express Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.					
ACCESSION		CL957492					
VERSION		CL957492.1 GI:52369867					
KEYWORDS		GSS.					
SOURCE		Oryza sativa (indica cultivar-group)					
ORGANISM		Oryza sativa (indica cultivar-group)					
REFERENCE		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.					
AUTHORS		Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.					
TITLE		An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis					
JOURNAL		Unpublished (2004)					
COMMENT		Contact: Chen Chen Department of Bioinformatic Beijing Institute of Genomics Chinese Academy of Sciences, Beijing 101300, China Tel: 86-10-80481559 Fax: 86-10-80488676 Email: chenchen@genomics.org.cn Rice genomic sequence. Class: exon-trapped.					
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[illegible]

Db	568	ATTACAGCAATATGAACAGAGGATGCCACTCATTTATGTCRAATATATATACCTACCAGA	627
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Db	1048	TTTTTTCACAAAGGATGCTTCAGAGCTATAGATCTCGCTTTCAGCTTGGCTCCAGT	1107
Qy	1085	CACCAAGTCTAGCTGCACTGGCTCGAAGCATGTCTCATCGCTTTTCAATGAATCC	1144
Db	1108	CACCAATCTAGATGCACTGTCTTGAAGCTGTGCAATCATCTTTGATGAGTGC	1167
Qy	1145	GAGAGCAAAACCCCGCTTTCCAAATGGTGGTCCATTTACCGCATTTGTTCAATTTCA	1204
Db	1168	GAGAACCAATCGAGGTTTGCCAAATGGACGCCATTTCTCCATGTTTCACTTTAAAC	1227
Qy	1205	AGAGTTAGTGGAGCTTCAATGGAGCTAATCAAGGCTATACCTGAGCATGTGAGAC	1264
Db	1228	AGGAATAGCAAAATGCTCCAGAGCTCATCAAGGCTGTATCCAGACCATGCTAGGC	1287
Qy	1265	GACA 1268	
Db	1288	GGCA 1291	
RESULT 5			
LOCUS AY104068			
DEFINITION Zea mays PC083097 mRNA sequence.			
ACCESSION AY104068			
VERSION AY104068.1 GI:21207146			
KEYWORDS HTC.			
SOURCE Zea mays			
ORGANISM Zea mays			
REFERENCE 1 (bases 1 to 1666)			
AUTHORS Hailey C.F., Dolan M., Miao G.H., Vogel J.M., Whiteitt, M.S.,			
TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of			
JOURNAL Overgo Probes			
REFERENCE 2 (bases 1 to 1666)			
AUTHORS Arthur L.W., Hanafey M., Morgante M. and Tingey S.V.			
TITLE Maize Mapping Project/Dupont Consensus Sequences for Design of			
JOURNAL Unpublished (2002)			
REFERENCE 3 (bases 1 to 1666)			
AUTHORS Coe E.H.			
TITLE Direct Submission			
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of			
Missouri, Columbia, MO 65211, USA			
If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.			
FEATURES			
Location/Qualifiers			
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/organism="Zea mays"			
/mol_type="mRNA"			
/db_xref="MaizeDB:634655"			
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/clone_lib="Maize Mapping Project/Dupont Consensus Library"			
/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed Dupont contigs; this resource was assembled by Dupont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"			
ORIGIN			
Query Match 41.2%; Score 665; DB 3; Length 1666;			
Best Local Similarity 75.4%; Pred. No. 7.3e-162;			
Matches 827; Conservative 0; Mismatches 270; Indels 0; Gaps 0;			
Qy	199	GAGGCAATGACGCTGTACTGTCATATCATTTCCACTACTATAGGAGGCAAAACGCG	258
Db	260	GAAGGGGAGAGCTGTGACGGTCAATCATCTCCACCACCATCGCGGGAGAACGCG	319
Qy	259	GAACCAAGACGACCATTTAGTTACATGCTGAGCGGTTGTTGGAACAGGTTTCATTCGG	318
Db	320	GAGCCAAAGCGACCATCAGTTACATGTCAGAACGTCGTGGTACGGGCTCATTTGGG	379
Qy	319	ATTGTTTTTTCAGCGAAATGCTTGAACACTGAGAAATCAGTAGCCATTAAGAGGTCCTG	378
Db	380	ATCGCTTTCCAGGCTAAGTGTGAGAGCTGAGAGACCTTCGCCATTAAGAGGTCGTG	439
Qy	379	CAAGATCGACGCTATAAAACCGTCAGTTGCAACTTAATGCGACCAATGATGATCCCAAT	438
Db	440	CAGGATCGGCTTACAGAACCGGAGCTGCAACTTATGCGTGCCATGAGCACCACAC	499
Qy	439	GTCACTCTCTTGAACACTGTTTCTTCTCAACAGAGTAGAGATGAGCTTTCCTCAAC	498
Db	500	GTCACTCTCTTGAACACTGTTTCTTCTCAACAGAGTAGAGATGAGCTTTCCTCAAC	559
Qy	499	CTGTATGAGATGATGATACCTGAGACTTTATACCGGGTTTGGAGGACTATATAGTTCT	558
Db	560	CTTGTATGGAATTTGTCCCGAGACCTGTACCGTGTCTGAAGCACTACAGCAACGCG	619
Qy	559	AATCAGAGATGCCAATTTTCTATGCAAGCTTTTACACATATCAATCTTTAGAGGTTTG	618
Db	620	AACAGAGATGCTCTTATCTACGCTCAAGCTCTACATGATCAGCTTTTCAGAGGCTTA	679
Qy	619	GCTTACATCCATCTGTTCCCGGTTTGGCCACAGAGATGTGAAGTGTGCTTCTTGGT	678
Db	680	GCTTATATTCATATGATACAGGAGTCTGCCATAGGATGTAAAGCCCAAAACGTTTG	739
Qy	679	GTTGATCCCTTGACCCATCAGGTTAAGCTGTGTGATTTTGGAGTGTGCAAAAGTATGGT	738
Db	740	GTTGATCTCTCACCCACGAGTCAAGCTCTGTGACTTTGGTAGGCAAAAGTCTCTGAT	799
Qy	739	AAAGGTGAACCAACATATATATCTGCTCCGTTATTCGCTTATTCGCTCCCAAGCTCAT	798
Db	800	CTGTGTGAACCAACATATCTTACATATATGCTCTCGTTATTCGCTTATTCGCTTAT	859
Qy	799	TTTGGCGCCACAGATATACAGCATCCATAGATATATGCTCTGCTGTTGTGTACTGGCA	858
Db	860	TTTGGAGCGAGGAGTATACAACTTCAATAGACATATGCTGAGCTGGCTGTCTTAGCT	919
Qy	859	GAGCTTCTTCTTGGCCGCGCTTATTTCCAGAGAAATTCAGTTGATCAGCTTGTGGAG	918

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Db 920 GAGTGTCTTCTGGTCAGGCACCTGTTTCGGGAGAGAGTGCTGTTGATCAGTTGGTAGAG 979
Qy 919 ATCATAAAGTCTTGGTACTCAACTCGTGAAGAAATTCGATGATGAACCCGGAACCTAC 978
Db 980 ATTATCAAGGTTCTGGTACTCAACCCGCTGAGGAGATACGATGCAATCCCAACTAT 1039
Qy 979 ACAGATTTAGGTTCCACAAATCAAGCTCACCTTCGACAAAGGTTTTCATAAACGG 1038
Db 1040 ACTGAGTTCAGGTTCTCAGATAAAGGCTCATCCGTGGCACAAGATTTCCACAAGAGA 1099
Qy 1039 ATGCTCCAGAACATAGACCTTGACATCTCGGCTTCTTCAATATTCACCAAGCTTACGC 1098
Db 1100 ATGCTCCTCAAGCCATTGACCTTGCTCTCGTCTCTTTCAGTATTCACCAAGCTTTCGC 1159
Qy 1099 TGCACTGCGCTCGAAGCATGTGCTCATCGGTTTTCATGAATCCGAGAGCAAAACGCC 1158
Db 1160 TGCTCTGCTCTTGACGCATCGCTCATCCCTTCGATGAGCTGGGACACCGAACGCA 1219
Qy 1159 CGTCTTCCAAATGCTCGTCCATTACCGCCATTGTTCAATTTCAAAACAGATTTAGCTGGA 1218
Db 1220 CGCTTACAAACGCGCCGCTTCCCTCCGCTCTTAACTTCAAGCACCAACTAGCAAT 1279
Qy 1219 GCTTCAATGAGCTAATCAACAGGCTAATACCTGAGCATGTGAGACGACAAATGAGCACA 1278
Db 1280 GCCTCTCGGACCTCGTACGAGGCTTGTCGCGGAGCACATTAGACGCGATCGGTGTC 1339
Qy 1279 GGATTCAAAACAGTTA 1295
Db 1340 AACTTCGGGAGCAGCTA 1356

RESULT 6
CK266410
LOCUS
DEFINITION
EST712488 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone POAC457 5' end, mRNA sequence.
CK266410
CK266410.1 GI:39823388
EST.
Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 924)
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
1. .924
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POAC457"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-TonA"
/clone_lib="potato abiotic stress cDNA library"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,

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6hr, 12hr, 1d, 2d, and 4d; roots:2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots:3d
and 5d). Set 3 were grown under the standard conditions
and then were cold stressed by placement at 4 C. Cold
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d. Set 4 were grown under the standard conditions and
then were heat stressed by placement at 35 C. Heat
stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,
2d and 4d and heat-stressed roots were harvested at 6 hr,
12 hr, 1 d, and 4d. RNA was isolated from all tissues and
equal RNA from each tissue and stress was pooled to
construct the cDNA library. RNA sample."

ORIGIN
Query Match 39.4%; Score 635.4; DB 7; Length 924;
Best Local Similarity 80.8%; Pred. No. 3.3e-154;
Matches 741; Conservative 0; Mismatches 176; Indels 0; Gaps 0;

Qy 308 GTTCATTCCGGATGTTTTTCAGGGGAAATGTTGGAACTGGAGAACTCAGTAGCCATTAA 367
Db 1 GGTCTCTTGGGATAGTGTTCAGGCAAAATGCTTGGAACTGGAGAGACTGTGGCCATAA 60
Qy 368 AAAGGCTCTGCAAGATCGACGCTATAAAACCGTGAGTTGCAACTAATGCGACCAATGG 427
Db 61 AGAAGGTTTTTCAGGACAAGCGGTATAAAACCGTGAACTACAACCTGATGCGCTTATGG 120
Qy 428 ATCACCCTAAATGTCATCTCTTGAAGCACTGTTTCTTCTCTACAAACGAGTAGAGATGAGC 487
Db 121 ATCACCCTAAATGTCATCTCTTGAAGCACTGTTTCTTCTCTACAAACGAGTAGAGATGAGC 180
Qy 488 TCTTCCTCAACCTGTTATGAGATGATGACTGAGACTTTTATACCGGGTTTGGAGCACT 547
Db 181 TTTTCTTAATTTGGTGCATGATATGTCCTGAAAGTTTATACAAAGTTTAAAGCACT 240
Qy 548 ATACTAGTTCTAATCAGAGATGCCAATTTCTATGTCAAGCTTTTACACATATCAATCT 607
Db 241 ATAGCAATTTCAATCAAGGATGCCACTCATATATGTCAAACTTTTACATGTATCAGATAT 300
Qy 608 TTAGAGGTTTGGCTTACATCCATCTGTTTCCCGGTGTTTGGCCACAGAGATGTGAACCCAC 667
Db 301 TCAGAGGCTGCTTACATCTATATGTTCCAAAGATTTGCCATAGAGATGTGAACCTC 360
Qy 668 AAAATCTCTGTTGATCCCTTGACCCATCAAGCTTAAGCTGTGATGTTTGGAAAGTGCAA 727
Db 361 AAAATCTTTTGGTTGATCCTCTGACCCATCAAGCTCATGTGATTTTGGAAAGTGCAA 420
Qy 728 AAGTATTGCTCAAGGTGAACCAACATATATATCTGCTCCCGCTTATATCGTGCTC 787
Db 421 AAGTCTCTGTTGATGTTGAGCAAAATTTTCGTACATTTGCTCTCCTACTACAGAGCTC 480
Qy 788 CAGAACTCATCTTTTGGCGCCACAGAGATATACAGCATCCATAGATATATGCTCTGCTGGTT 847
Db 481 CAGAACTCATATTTGGTGCACAGATATACACATCAATTTGATATTTTGGTCAAGAGCT 540
Qy 848 GTGTACTGGCAGAGCTTTCTTTTGGCCAGCGTTATTTCCAGAGAGAAAATTCAGTTGATC 907
Db 541 GTGTCCTTGTGAGCTTTCTTCTGGGCGAGCGCTCTTCTGCGGCAAAATTCGCGTAGACC 600
Qy 908 AGCTTGTGAGATCATAAAGGTTCTTGGTACTCCAACTCGTGAAGAAATTCGATGTATGA 967
Db 601 AACTGTGTGAGATCATCAAGGTTCTTGGTACTCTCTACTCGGGAAGAAATTCGATGTATGA 660
Qy 968 ACCCGAACTACACAGATTTTAGGTTTCCCAAAATCAAGCTCACCTTGGCACAAGTTT 1027
Db 661 ACCCAACTACACAGATTTTCAAGTTCCACAGATATAAGCTCATCTTGGCACAAGGAT 720
Qy 1028 TTCAATAACGAGATGCTCCAGAGCAATAGACCTTCGATCTCGGCTTCTTCAATATTCAC 1087
Db 721 TCCATAAAAGAAATGCTCTCTGAAGCAATTTGATCTTGCCTCACGGCTTCTTCAATATTCAC 780

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Db 1 CGAAGGATCAGATATGACGGAGTCGAAGCAACCGCTCACCGGACATATCATCTCTACT 60
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Db 61 ACAATTTGAAGGGAAGAAATGCTGAACCAAGAGAGCGATAGCTATATGCTGAGCGCAT 120
QY 298 GTTGGACAGGTTTCATTCGGGATGTTTTTTCAGGGAATGCTTGGAACTCGGAATCA 357
Db 121 GTGGGAACCTGGGTCATTTGGAATGTTCTCCAGGCAAAATGCTTGGAAACAGGGAGACT 180
QY 358 GTAGCCATTAATAAAGGCTTTGCAAGATCGACGCTATAAAAAACCGTGAGTTGCAACTAATG 417
Db 181 GTTGCCATAAAGAGGTGTTGGGACAGAGATACAGAACTCGGAGGTTCAATTGATG 240
QY 418 CGAACCAATGGATCACCCAAATGTCTCTCTTGAAGCACTGTTTCTCTCTACACGAGT 477
Db 241 CGACGATGGATCATCTAATGTTGTTCTTAAAGCACTGTTTTTCTCGACCAACAGC 300
QY 478 AGAGATGAGCTCTTCTCTCAACCTGTTTATGGAGTATGTACCTGAGACTTTATACCGGTT 537
Db 301 AGAGACGAGCTTTTCTCAACCTGGTCATGGAGTTTGTGCTGAATCTTTTATACCGAGTT 360
QY 538 TTGAGGCACTACTAGTTTCTAATCAGAGATGCCAAATTTCTATGCTCAAGCTTTTACACA 597
Db 361 CTTAGCATATATAGTATGATGAACAGAGATGCCAATGATATTTGTGAGCTCTATACC 420
QY 598 TATCAAACTTTAGAGGTTTGGCTTATACATCCATCTGTTCCCGGTTTGGCCACAGAGAT 657
Db 421 TATCAGATTTTCCAGGGGGTAGCTTATATTCATAGTGTCCAGGAGTTTGGCCATAGAGAT 480
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Db 481 GTGAAGCCCAAAATGTTCTGTTGATGCTCTCACTCACCAAGTTAAGCTTTGTGATTTT 540
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Db 541 GGAAGGCCAAATTTCTGTTAAGGTGAAGCAACATATCTTACATTTGTTCCAGCTAT 600
QY 778 TATCGTGCTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGCATCCATAGATATAGG 837
Db 601 TATCGTGCTCCGNACTTATATTTGGGGCGACAGAGTACACTACTTCTTATGACATATGG 660
QY 838 TCTGCTGTTGTTGTTACTGACAGCTTCTTCTTGGCCAGCGGTTATTTCCAGGAGAAAT 897
Db 661 TCAGCAGGCTGTGCTCTGAGTTACTCTCTTGGCGCAGAGTACACTACTTCTTCCGAGAAAT 720
QY 898 TCAGTTGATCAGCTGTGGAGATCATAAAGTTCTTTGTTACTCCAACCTCGTGAAGAAAT 957
Db 721 GCTGTTGATCAGCTGTGGAGATTAATCAAGGTTCTTGGTACTCCAACCTCGGAGGAAAT 780
QY 958 CGATGTATGAACCCGAACTACACAGATTTTATAGTTTCCCAAAATCAAAGCTCACCCCTGG 1017
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QY 1018 CACAGGTTTTTTCATAAAGGATGCTTCCAGAGCAATAGACTTGCATCTCGGCTTCTT 1077
Db 841 CATAGATATTCACAAGAGAAATGCCACAGAGCAATAGATCTTACATCAGCACTTCTC 900
QY 1078 CAATATTCACCAAGTCTACGCTGCATGC 1106
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RESULT 10
CL964803
LOCUS
DEFINITION
OsiFCC011089 Oryza sativa Expressed Library Oryza sativa (indica cultivar-group) genomic, genomic survey sequence.
ACCESSION
CL964803
VERSION
CL964803.1
KEYWORDS
GSS.
Oryza sativa (indica cultivar-group)
SOURCE
Oryza sativa (indica cultivar-group)
ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzoideae; Oryza.
REFERENCE
AUTHORS
1 (bases 1 to 2295)
Ma, L., Wang, J., Chen, C., Liu, X., Su, N., Li, L., Wang, X., Cao, M., Jiao, Y., Sun, N., Zhang, X., Bao, J., Sun, D., Zhao, H., Yuan, L., Wong, G. K. S., Deng, X. W. and Wang, J.
An analysis of transcriptional regulation of the rice genome and its comparison to Arabidopsis
Unpublished (2004)
JOURNAL
COMMENT
Contact: Chen Chen
Department of Bioinformatic
Beijing Institute of Genomics
Chinese Academy of Sciences, Beijing 101300, China
Tel: 86-10-80481559
Fax: 86-10-80488676
Email: chenchen@genomics.org.cn
Rice genomic sequence.
Class: exon-trapped.
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location/Qualifiers
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/clone_lib="Oryza sativa Expressed Library"
/note="Oryza sativa exon trapped genomic sequences"
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Best Local Similarity 76.0%; Pred. No. 8.5e-139;
Matches 711; Conservative 0; Mismatches 224; Indels 0; Gaps 0;
QY 186 TCGAGCTGTTATTGAGGAAATGACGCTGTCTGATCATATCATTTCCACTTACTATAGG 245
Db 117 TCCCACTAATATGGAGGAATGATCCAGTCACAGTCATATAATTTCAACTACTATTGG 176
QY 246 AGGCAAAAACGGCAACCAAGCAGACCATTAGTTTACATGCTGAGCGGTTGTTGGAC 305
Db 177 AGGGAAGAACCATGAGCCCAAAAGGACTATTAGCTATATGCTGAACGAGTTGTTGGAA 236
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Db 237 TGGATCTTTGGTGTGTTATTCAGGCAAAATGCTTGGAGCTGTGAACTGTTGCCAT 296
QY 366 TAAAAAGTCTTGAAGATCGACGCTATAAAACCGTGAGTTGCAACTAATCGCACTAT 425
Db 297 TAAGAAGTCTTTACAGGACAAACGATACAGAAACAGAGATTACAGATAATTCGATCAAT 356
QY 426 GGATCACCCAATGTCTCTCTTGAAGCACTGTTTCTTCTACACAGAGTAGATGA 485
Db 357 GGATCATTCGAATGTCTCTCCCTTAAAGCAATGTTTCTTCTTACCAACAGAGATGA 416
QY 486 GCTCTCTCAACCTGTTTATGGAGTATGATCCTGAGACTTTTATACCGGTTTTCAGGCA 545
Db 417 ACTTTTCTTAACTTAGTCATGGAGTTTGTCCGAGTCACTTATCGTCTCTGAAACA 476
QY 546 CTATATAGTTCTAATCAGAGATGCCAATTTTCTTATGTCAAGCTTTTACATATCAAT 605
Db 477 CTACAAGATATGAAGCAGAGATGCCAATTTATATGTCAAACTTTTATCATGTATCAGAT 536
QY 606 CTTTGAAGTTTGGCTTACATCCATCTGTTCCCGGTTTGGCCACAGAGATGTGAACC 665
Db 537 ATTCCGCGGATTTAGCTTACATTCACACTGTTTCTAGAGTTTGTCTACCGAGATATAAGCC 596
QY 666 ACARAATCTTGGTTGATCCCTTGACCCATCAGCTTAAGCTGTGATTTTGGAGTGC 725
Db 597 ACAAATATCTTGGTTGATCTCTTTACCACCAAGTGAAGGTTCTGTGATTTTGGAGTGC 656
QY 726 AAAAGTATTGGTCAAAAGGTGAACCAACATCATATATCTGCTCCCGTTTATTCGTGC 785
Db 657 TAAATGCTGATTAAGGTGAAGCAATATATCTTACATATGCTCACGCTTACTATCGTGC 716
QY 786 TCCAGAACTCATCTTTTGGCGCACAGAGTATACAGATCCATAGATATATGCTGCTGTCG 845


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Db      717 TCCTGAGCTCATATTTGGTGCAACTGAGTACACAAATCAATGATATATGTCCTGCG 776
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Db      777 ATGTGTCTTGGCTGAGCTGCTTCTGGTCAACCTCTGTTTCTCTGGTGAAAGTGCAGTGA 836
Qy      906 TCAGCTTGTGGAGATCATAAAGGTTCTTGGTACTCCAACTCGTGAAGAAATTCGATGTAT 965
Db      837 CCAGCTTGTGGAGATTAATTAAGGTTTGGGTACTCCAAACGCGAGAGAAATTCGGTTGAT 896
Qy      966 GAACCCGAACTACACAGATTTTAGGTTCCCAAAATCAAAGCTCACCCCTTGGCACAAGGT 1025
Db      897 GAATCCCAATTCACAGAAATTCAAATTCGCGAGATAAAGCATGCCATGGCACAAGAT 956
Qy      1026 TTTTCATAAAGGATGCTCCAGAGCAATAGACCTTGCATCTCGGCTTCTTCATATTC 1085
Db      957 CTTCACAGCAAGATGCTCCCAAGCAATAGATCTTGTGTCCTCGTCTCTTCAGTATTC 1016
Qy      1086 ACCAAGCTACGCTGCACTGCGCTCGAAGCATGTG 1120
Db      1017 GCCAAATCTCGATGTAATCTCGGATTCGCAAGGG 1051

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RESULT 11
 CK290108
 LOCUS
 DEFINITION
 EST752830 Nicotiana benthamiana mixed tissue cDNA library,
 normalized, full-length Nicotiana benthamiana cDNA clone NBMS53 5',
 end, mRNA sequence.

ACCESSION
 CK290108
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

Nicotiana benthamiana
 Nicotiana benthamiana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiids; Solanales; Solanaceae; Nicotiana.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

The Institute for Genomic Research
 9712 Medical Center Dr, Rockville, MD 20850, USA
 Email: potato-array@tigr.org
 Clones can be requested from the University of Arizona Genomics
 Institute via http://genome.arizona.edu/orders/
 Seq primer: ATT TAG GNG ACA CTA TAG.

FEATURES
 source

1. 910
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 /db_xref="taxon:4100"
 /clone="NBMS53"
 /tissue_type="abiotic and biotic stress-treated leaves,
 callus tissue and root tissue"
 /lab_hosts="DH10B-Tona"
 /clone_lib="Nicotiana benthamiana mixed tissue cDNA
 library, normalized, full-length"
 /notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
 supplier: RNA was isolated from Nicotiana benthamiana
 tissues that include callus, roots from liquid culture
 grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
 cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
 challenged leaves (Pseudomonas syringae pv tomato 12 hr;
 Xanthomonas campestris pv campestris 12 hr, 18hr;
 Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
 campestris pv vesicatoria 18hr). RNA was isolated from
 these tissues and pooled in approximately equal molar
 amounts."

ORIGIN

Query Match 35.6%; Score 575; DB 7; Length 910;
 Best Local Similarity 77.7%; Pred. No. 1.8e-138;
 Matches 695; Conservative 0; Mismatches 200; Indels 0; Gaps 0;

Qy 164 TGGATTCTGATAAGGAAATGTCTGACAGCTGTTATTATGAGGAAATGACGCTGTGTACTGGTC 223
 Db 16 TGGCTGATGATAAGGAGATGTCTGCTCTGTTATGATGTGAATGCTGTCAGTCACCTGGTC 75
 Qy 224 ATATCATTTTCCACTACTATAGAGGCAAAACGGGCAACCAAGCAGACCATATTAGTTACA 283
 Db 76 ATATAATTTCCACTACCATCGGAGGAGAAATGGCGAGCCAAAGCAGACAGTCAGTTACA 135
 Qy 284 TGGCTGAGCGGGTGTGTGAACAGGTTCAATTCGGGATTCGTTTTCAGGCGAAATGCTTGG 343
 Db 136 TGGCTGAACGTGTGCTGGGAGCTGGATCAATTTGGAGTTGTTTTTCAAGCAAAATGCTTGG 195
 Qy 344 AAACCTGGAGAATCAGTAGCCATTAAAGAGTCTTGAAGATCGACGCTATAAAACCGTG 403
 Db 196 AAAACGGGAGACAGTGGCAATAAAGAGGTTTTACAAGATCGTAGATCAAGAATCGTG 255
 Qy 404 AGTTGCAACTAATGCGAACCAATGGATCACCAAAATGTCAATCTCTTGAAGCAGCTGTTTCT 463
 Db 256 AACTGCAGTTAATGCGCACAATGGATCACTCGAATGTTGTTTTTAAAGCATTTGCTTCT 315
 Qy 464 TCTCTACAAACGAGTAGAGATGAGCTCTTCTCAACCTGCTTATGGAGTATGTACCTGAGA 523
 Db 316 ATTCAACTACTAGTAAAGAGAGCTTTTCTCAATTTAGTCATGGAATATGTTCCAGAAA 375
 Qy 524 CTTTATACCGGGTTTTGAGGCACATACATAGTTCTAATCAGAGGATGCCAATTTTCTATG 583
 Db 376 CCATGTACCGCATGTTGAAGCATTAACAGCAATGCGAAACCAAGATGCCAATCATCTATG 435
 Qy 584 TCAGCTTTACACATATCAAACTTTAGAGGTTTGGCTTACATCTACTGTTCCCGGTG 643
 Db 436 TTAAGCTTTACACATATCAAGTATTTAGGGGGCTGGCATACTACACAGTTGCTGGCG 495
 Qy 644 TTTGCCACAGAGATGTGAACACCAAAATCTCTTGGTGTGATCCCTTGACCCATCAGGTTA 703
 Db 496 TTTGCCACAGAGATTTGAAACCTCAGATAATTTTAGTTGACCTGTTACTCACCAGTCA 555
 Qy 704 AGCTGTGTGATTTTGGAGTGCAAAAGTATTTGTCAAAGGTGAACCAACATATCATATA 763
 Db 556 AAATTTGTGATTTTGAAGTGCAAAAGTACTGTTAAAGGTGAAGCAACATCTCGTACA 615
 Qy 764 TCTGCTCCGCTTATTTATGCTGCTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGCAT 823
 Db 616 TCTGCTCGCGGTTTTATCGAGCTCCTCGAACTGTATTTTGGTGGCAGAGTATACTACCT 675
 Qy 824 CCATAGATATATGCTGCTGCTGGTTGTGTACTGGCAGAGCTTCTTCTTGGCCAGCGGTTAT 883
 Db 676 CTATTGATATCTGGTCGGCTGGCTGTCTTGGCCAGGCTCTCTCTCGGCGAGCCATTAT 735
 Qy 884 TTCAGGAGAGAAATTCAGTTGATCAGCTTTGTGGAGATCATAAAGGTTCTTGGTACTCCAA 943
 Db 736 TTCAGGAGAGAAACGCTGTCGATCAGCTTGTGAGATAATCAAGGTACTTGGAACTCCAA 795
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 Db 796 CRAAGGAGGAAATTCGCTGTATGAATCCAAATTTACATGATTTTGGTTTCCGCAATCA 855
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 Db 856 AAGCGCACCTTGGCATTAGGTATTCCACACAGCAATGCCACCTGAAGAGCTAGA 910

RESULT 12
 CNS09YSF
 LOCUS
 DEFINITION
 Arabidopsis thaliana Full-length cDNA Complete sequence from clone
 GSLTUS91ZE05 of Adult vegetative tissue of strain col-0 of
 Arabidopsis thaliana (thale cress).
 ACCESSION
 BX831446

CNS09YSF 1638 bp mRNA linear HTC 06-FEB-2004
 Arabidopsis thaliana Full-length cDNA Complete sequence from clone
 GSLTUS91ZE05 of Adult vegetative tissue of strain col-0 of
 Arabidopsis thaliana (thale cress).
 ACCESSION
 BX831446

VERSION	BT31446.1	GI:42455013	Db	624	ACTGAAAAGATGAGCTTTACCTCAATCTTGTCTTGTAGTAGCTTCCAGAAACTGTTCAAT	583
KEYWORDS	HTC; GSLT; CDNA..		Qy	532	CGGGTTTTGAGGCACATATCTAGTTCTTAATCAGAGGATGCCAATTTTCTATGTCAAGCTT	591
SOURCE	Arabidopsis thaliana (thale cress)		Db	684	CGTGTATCAAACTACAAACAACTGAATCAGAGATGCTCTTATATGCGTCAAACTT	743
ORGANISM	Arabidopsis thaliana		Qy	532	TACACATATCAAACTTTAGAGGTTTGGCTTACATCCATCTGTTCCCGGTGTTGCCAC	651
REFERENCE	Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C., Menard, M., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.		Db	744	TACACTTATCAGATCCTTAGAGCCTTATCTTACATTCACCGATGCAATTTGGTGTGTGTCAT	803
AUTHORS	Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation		Qy	652	AGAGATGTGAAACCAACAAATCTCTTGGTTGATCCCTTGGACCATCAGGTAAAGCTGTCT	711
TITLE	Unpublished		Db	804	CGTGACATATAAACCTCAAAACTTGTGTAAATCCGCACACTCATCAAGTAAGCTATGT	863
JOURNAL	2 (bases 1 to 1638)		Qy	712	GATTTTGAAGTGCAAAAGTATTTGGTCAAGGTGAACCAAAATATCATATATCTGCTCC	771
REFERENCE	Genoscope.		Db	864	GGTTTTGGAAGTGCAAAAGTATTTGGTAAAGGAGAACCAAACTTTCTTACATCTGCTCG	923
AUTHORS	Direct Submission		Qy	772	CGTTATTATCGTCTCCAGAACTCATCTTTGGCGCCACAGAGTATACAGCATCCATAGAT	831
JOURNAL	Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage ; BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)		Db	924	AGGTATTACAGAGCACCTGAACTCATCTTTGGAGCAACCGAGTATACGACAGCCATTGAT	983
COMMENT	The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M. URV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/banque_Projet_EF/Full length http://www.genoscope.cns.fr/cgi-bin/ggb?ggb?source=Arabidopsis.		Qy	832	ATATGCTCTGCTGGTGTGTACTGCGCAGAGCTTCTTTGGCCAGCGTATTTTCCAGGA	891
FEATURES	Location/Qualifiers		Db	984	GTCGTGCTGCGAGGATGTTCTAGCTGAACATTTGCTTGGACAGCCCTTGTTCCTGCT	1043
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0; Mismatches	/plasmid="pCWSFORT_6"		Db	1224	CTTCTTCAATATTCACCAAGTCTAGCTGCACTGGCTCGAGCATGTGCTCATCGTTT	1283
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352	GAATCAGTAGCCATTAATAAGGTTCTTGAAGATCGACGCTATATAAACCGTCAGTTGCA	411	DEFINITION			
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			ORGANISM			
			Arabidopsis thaliana (thale cress)			
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			1 (bases 1 to 591)			
			Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.			

TITLE Large scale analysis of Arabidopsis full-length cDNA (2002b)
JOURNAL Unpublished (2002)
COMMENT Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-9060
Email: meeki@rkc.riken.go.jp
An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.

FEATURES
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/organism="Arabidopsis thaliana"
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ORIGIN
Query Match 35.5%; Score 572.2; DB 1; Length 591;
Best Local Similarity 99.2%; Pred. No. 8.9e-138;
Matches 58; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
Qy 48 GAGAGAGAAAGAGTAAAAAGCACATGGCCTCATACATTGGGGCCTCAGCCTCATGC 107
Db 2 GAGAGAGAAAGAGTAAAAAGCACATGGCCTCATACATTGGGGCCTCAGCCTCATGC 61
Qy 108 TCTTGCTCCGCGTGCAGCTTACGACGGCGAGCGCTTGAACGGCGCTCTGAATGGA 167
Db 62 TCTTGCTCCGCGTGCAGCTTACGACGGCGAGCGCTTGAACGGCGCTCTGAATGGA 121
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Db 122 TTCTGATAAGGAATGCTCGAGCTGTATTGAGGGAATGACGCTGTACTGCTCATAT 191
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Qy 468 TACAACAGTAGAGATGAGCTCTTCTCAACCTTGTATGGAGTATGATCTAGAGCTTT 527
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Qy 528 ATACCGGGTTTGAGGCACTATCTAGTCTTAATCAGAGATGCAATTTTCTATGTCAA 587
Db 482 ATACCGGGTTTGAGGCACTATCTAGTCTTAATCAGAGATGCAATTTTCTATGTCAA 541
Qy 588 GCTTTACACATATCAAAAT-CTTTAGAGGTTTGGCTTATCCATCATCTGTT 636
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Db 542 GCTTTACACATATCAAAATCCTTTAAAGGTTTGGCTTACATTCATCTGTT 591

RESULT 14
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DEFINITION CB971865 829 bp mRNA linear EST 30-APR-2003
Vitis vinifera cDNA clone CAB10006_IIia_Fa_H05 5', mRNA sequence.
CB971865
ACCESSION CB971865.1 GI:30255733
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 829)
AUTHORS Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leslie,A., Xu,J., Jones,K. and Cook,D.
TITLE Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon' berries at various developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGGTACCGGACATATGCC.
FEATURES
Location/Qualifiers
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/note="Organ: Flower - Pre-bloom; Vector: pDNK; Site_1: Sfil; Site_2: Sfil; CAB1 is a cDNA library of Vitis vinifera cv. 'Cabernet Sauvignon' Clone 8 flowers. Samples were collected approximately eleven days before onset of bloom (clusters at this stage were fully developed and flowers with calyptras or caps still attached. Sampled vines were located at the University of California, Davis, Experimental Vineyard. cDNAs were made by oligo-dT priming and directionally cloned. 5' and 3' adaptors were used in cloning as follows:
5'-ATGCTGTTGTTTACGAGTGGCCATTACGCGCGG-3' and
5'-ATCTAGAGCGGAGCGCGGACATG-dT(30)NN-3'. Library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-3 kb size fraction."

ORIGIN
Query Match 35.4%; Score 572; DB 6; Length 829;
Best Local Similarity 80.8%; Pred. No. 1.1e-137;
Matches 668; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
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Qy 377 TGCAAGATCGACCTATAAAACCGTGAGTTGCAATTAATGCGACCAATGATCAACCAA 436
Db 61 TGCAGGACAGAGATATAGAAATCGTGAGTTAATGCGACGATGATCATCAA 120
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Db 121 ATGTCGTTTTCCCTAAAAACATTTGTTTCTTCTTACTACAGTAGAGATGAGCTTTTCTCA 180
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 Db 181 ACTTGTATGAATATGTCCTGAGACTATGATCGGGTCTGAGCACTACAGCAATG 240
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 Db 241 CAAAACAGCAATGCTCTTATATATGTGAATTTTACATCTACCAATTTTCAGGGGCC 300
 QY 617 TGGCTTACATCANACTGTTCCGGGTGTTGGCCACAGATGTGAAACACCAAAATCTCT 676
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 QY 677 TGGTTGATCCCTTGACCCATCAGTTTAAGCTGTGATTTTGGAGTGCABAAGTATGG 736
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 QY 857 CAGAGCTTCTTCTGSCCAGCGGTTATTTCCAGGAGAAATTCAGTTGATCAGCTTGTGG 916
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AY108486 1752 bp mRNA linear HTC 16-OCT-2002
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 AY108486
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 1752)
 Hainey C.F., Dolan M., Miao G.H., Vogel J.M., Whiteitt, M.S.,
 Arthur L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
 Maize Mapping Project/DuPont Consensus Sequences for Design of
 Overgo Probes
 Unpublished (2002)
 2 (bases 1 to 1752)
 Coe, E.H.
 Direct Submission
 Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
 If you are interested in getting corresponding physical clones,
 these are publicly available from ZmDB and may be found by BLAST
 searching at MSL, maizenap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat

Schnable, Iowa State, then clones may be requested from ZmDB:
 www.zmdb.iastate.edu.
 Location/Qualifiers
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 assemblies resulting from the application of public
 contigs to seed DuPont contigs; this resource was
 assembled by DuPont as part of a collaboration for the
 overgo addressing of BACs in conjunction with the Maize
 Mapping Project"

ORIGIN

Query Match 34.2%; Score 551.4; DB 3; Length 1752;
 Best Local Similarity 70.9%; Pred. No. 3e-132;
 Matches 732; Conservative 0; Mismatches 301; Indels 0; Gaps 0;

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 QY 232 TCCACTACTATAGGAGGCAAAACCGCGAAACCAAGCAGACCATATTAGTTACATGCTGAG 291
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Db ||||| ||||| |||||
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